





PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books
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 PID g3004485
 VERSION CAA76561.1 GI:3004485
 DBSOURCE embl locus PPY16960, accession Y16960.1
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 ORGANISM Phleum pratense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poeae; Phleum.
 REFERENCE 1 (residues 1 to 53)
 AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
 Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
 TITLE Molecular, immunological and structural characterization of Phl p6,
 a major allergen and P-particle-associated protein from Timothy
 grass (Phleum pratense) pollen
 JOURNAL J. Immunol. In press
 REFERENCE 2 (residues 1 to 53)
 AUTHORS Vrtala,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
 Experimental Pathology, Wahringer Guertel 18-20, AKH, 1090 Wien,
 AUSTRIA
 COMMENT Related sequence: Z27090.
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books	
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DEFINITION Phl p6 IgE binding fragment [Phleum pratense].
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PID g3004473
VERSION CAA76560.1 GI:3004473
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Phleum.
REFERENCE 1 (residues 1 to 57)
AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
TITLE Molecular, immunological and structural characterization of Phl p6,
a major allergen and P-particle-associated protein from Timothy
grass (Phleum pratense) pollen
JOURNAL J. Immunol. In press
REFERENCE 2 (residues 1 to 57)
AUTHORS Vrtala,S.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
Experimental Pathology, Wahringer Guertel 18-20, AKH, 1090 Wien,
AUSTRIA
COMMENT Related sequence: Z27090.
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 DEFINITION Phl p6 IgE binding fragment [Phleum pratense].
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 PID g3004471
 VERSION CAA76559.1 GI:3004471
 DBSOURCE embl locus PPY16958, accession Y16958.1
 KEYWORDS .
 SOURCE timothy grass.
 ORGANISM Phleum pratense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poeae; Phleum.
 REFERENCE 1 (residues 1 to 80)
 AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
 Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
 TITLE Molecular, immunological and structural characterization of Phl p6,
 a major allergen and P-particle-associated protein from Timothy
 grass (Phleum pratense) pollen
 JOURNAL J. Immunol. In press
 REFERENCE 2 (residues 1 to 80)
 AUTHORS Vrtala,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
 Experimental Pathology, Wahringuer Guertel 18-20, AKH, 1090 Wien,
 AUSTRIA
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 PID g3004469
 VERSION CAA76558.1 GI:3004469
 DBSOURCE embl locus PPY16957, accession Y16957.1
 KEYWORDS .
 SOURCE timothy grass.
 ORGANISM *Phleum pratense*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poeae; Phleum.
 REFERENCE 1 (residues 1 to 106)
 AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
 Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
 TITLE Molecular, immunological and structural characterization of Phl p6,
 a major allergen and P-particle-associated protein from Timothy
 grass (*Phleum pratense*) pollen
 JOURNAL J. Immunol. In press
 REFERENCE 2 (residues 1 to 106)
 AUTHORS Vrtala,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
 Experimental Pathology, Wahringier Guertel 18-20, AKH, 1090 Wien,
 AUSTRIA
 COMMENT Related sequence: Z27090.
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 PID g3004465
 VERSION CAA76556.1 GI:3004465
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 ORGANISM Phleum pratense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poeae; Phleum.
 REFERENCE 1 (residues 1 to 138)
 AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
 Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
 TITLE Molecular, immunological and structural characterization of Phl p6,
 a major allergen and P-particle-associated protein from Timothy
 grass (Phleum pratense) pollen
 JOURNAL J. Immunol. In press
 REFERENCE 2 (residues 1 to 138)
 AUTHORS Vrtala,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
 Experimental Pathology, Wahringuer Guertel 18-20, AKH, 1090 Wien,
 AUSTRIA
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 VERSION CAA76557.1 GI:3004467
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 ORGANISM Phleum pratense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poeae; Phleum.
 REFERENCE 1 (residues 1 to 138)
 AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
 Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
 TITLE Molecular, immunological and structural characterization of Phl p6,
 a major allergen and P-particle-associated protein from Timothy
 grass (Phleum pratense) pollen
 JOURNAL J. Immunol. In press
 REFERENCE 2 (residues 1 to 138)
 AUTHORS Vrtala,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
 Experimental Pathology, Wahringner Guertel 18-20, AKH, 1090 Wien,
 AUSTRIA
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□1: Y16956. Phleum pratense m...[gi:3004466]

Related Sequences, Protein, Taxonomy

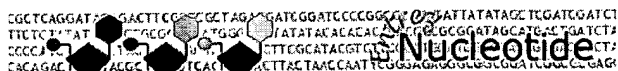
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DEFINITION Phleum pratense mRNA for Phl p6 allergen, isolate c142.
ACCESSION Y16956
VERSION Y16956.1 GI:3004466
KEYWORDS allergen; Phl p6 gene.
SOURCE timothy grass.
ORGANISM Phleum pratense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Phleum.
REFERENCE 1 (bases 1 to 571)
AUTHORS Vrtala,S., Fischer,S., Grote,M., Vangelista,L., Pastore,A.,
Sperr,W.R., Valent,P., Reichelt,R., Kraft,D. and Valenta,R.
TITLE Molecular, immunological and structural characterization of Phl p6,
a major allergen and P-particle-associated protein from Timothy
grass (Phleum pratense) pollen
JOURNAL J. Immunol. In press
REFERENCE 2 (bases 1 to 571)
AUTHORS Vrtala,S.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1998) S. Vrtala, Institute of General and
Experimental Pathology, Wahringer Guertel 18-20, AKH, 1090 Wien,
AUSTRIA
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☐ 1: Y16955. *Phleum pratense* m...[gi:3004464] [Related Sequences, Protein, Taxonomy, LinkOut](#)

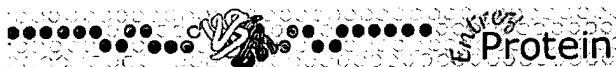
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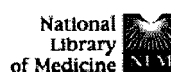


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LOCUS CAA81608 132 aa PLN 22-NOV-1995
 DEFINITION pollen allergen PhlpVI [Phleum pratense].
 ACCESSION CAA81608
 PID g414712
 VERSION CAA81608.1 GI:414712
 DBSOURCE embl locus PPRPHP1V, accession Z27082.1
 KEYWORDS .
 SOURCE timothy grass.
 ORGANISM Phleum pratense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poeae; Phleum.
 REFERENCE 1 (residues 1 to 132)
 AUTHORS Petersen,A., Bufer,A., Schramm,G., Schlaak,M. and Becker,W.M.
 TITLE Characterization of the allergen group VI in timothy grass pollen
 (Phl p 6). II. cDNA cloning of Phl p 6 and structural comparison to
 grass group V
 JOURNAL Int. Arch. Allergy Immunol. 108 (1), 55-59 (1995)
 MEDLINE 95375564
 REFERENCE 2 (residues 1 to 132)
 AUTHORS Petersen,A.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-1993) Petersen A., Forschungsinstitut Borstel,
 Allergology, Parkallee 22, 23845 BORSTEL, Germany
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PubMed1: J Allergy Clin Immunol 1996 Mar;97(3):781-7 Related Articles, [new Books](#), [LinkOut](#)

Immunologic characterization of purified recombinant timothy grass pollen (*Phleum pratense*) allergens (Phl p 1, Phl p2, Phl p 5).

PubMed
Services**Vrtala S, Susani M, Sperr WR, Valent P, Laffer S, Dolecek C, Kraft D, Valenta R.**

Institute of General and Experimental Pathology, University of Vienna, Austria.

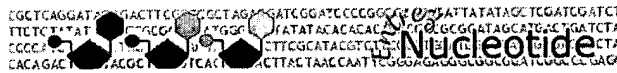
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BACKGROUND: Grass pollen allergens belong to the potent elicitors of type I allergy. Approximately 40% of allergic individuals display IgE reactivity with grass pollen allergens. In previous studies we have reported the complementary DNA cloning and expression in *Escherichia coli* of three of the most relevant timothy grass pollen allergens: Phl p 1, Phl p 2, and Phl p 5. **OBJECTIVE:** To achieve high level expression of immunologically active timothy grass pollen allergens in *E. coli*, the cDNAs were inserted into expression plasmids. **METHODS:** The three recombinant grass pollen allergens were expressed at high levels in *E. coli* as recombinant nonfusion proteins, purified by conventional protein chemical methods and tested for their IgE-binding capacity by immunoblot and ELISA, as well as in histamine release assays. **RESULTS:** Milligram amounts of pure recombinant allergens were obtained from cultured *E. coli*. IgE binding to purified recombinant Phl p 1, Phl p 2, and Phl p 5 could be demonstrated by immunoblot and ELISA. With ELISAs the percentage of grass pollen-specific IgE directed against the individual recombinant allergens could be estimated. In addition, the purified recombinant timothy grass pollen allergens induced dose-dependent and specific histamine release from patients' blood basophils. **CONCLUSION:** Purified recombinant timothy grass pollen allergens represent useful tools for diagnosis and therapy of grass pollen allergy.

PMID: 8613635 [PubMed - indexed for MEDLINE]

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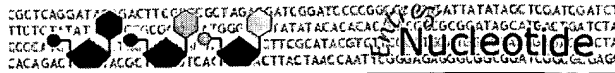
Show: 20
 Items 1-7 of 7
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1 of 2

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spand-sci-solam52 8 Nov 15 2001 10:41:10



1: Y16958. Phleum pratense m...[\[gi:3004470\]](#) [Related Sequences, Protein, Taxonomy, LinkOut](#)

BASE COUNT	184 a	141 c	110 g	137 t		
ORIGIN						
1	gcagacaagt	ataagacatt	cgaagccgcc	ttcacggtgt	cctcaaagag	aaacctcgct
61	gacgccggtt	caaaggcgcc	ccagctggtc	cccaagctcg	atgaagtcta	caacgccgcc
121	tacaatgctg	ccgatcatgc	cgccccagaa	gacaagtatg	aagccttcgt	ccttcacttt
181	tccgaggctc	tccacatcat	cgccggtacc	cccgaggatcc	agcgtgtcaa	gcccggcgcg
241	tagttgttca	gcacgggtcaa	gataccttgac	agcgctcgctg	ccaccgggcgc	tgcagccaac
301	actgccagtg	gctaaaaaat	tcgactagct	ccttcataca	atgaatacac	atgtatcatt
361	caaacatact	actgtacagt	atgtgcatga	cctagcggcg	agcatttttt	ttatgattaa
421	tcttttatac	atgggcgtga	tcgagcgtgt	gcataatgtgt	aataattaat	tttttatttt
481	gatttgaaat	tgtaatcctg	ataagaaatg	cgattaagtc	catttaaaaa	aaaaaaaaaa
541	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aa		

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 19, 2001, 13:09:45 ; Search time 11.59 Seconds
(without alignments)
407.874 Million cell updates/sec

Title: CAA76556
Perfect score: 138
Sequence: 1 MAAHKFWAMFLAVAVLGL.....SEALHIIAGTPEVHAVKPGA 138

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	80	58.0	132	1 MPP6_PHLPR	P43215 phleum prat
2	15	10.9	284	1 MP5B_PHLPR	Q40963 phleum prat
3	12	8.7	286	1 MP5A_PHLPR	Q40962 phleum prat
4	12	8.7	339	1 MP5B_LOLPR	Q40237 lolium pere
5	10	7.2	294	1 MP53_PHAHQ	P56166 phalaris aq
6	9	6.5	116	1 NU3M_STRPU	P15550 strongyloce
7	8	5.8	221	1 YG81_HAEIN	P44290 haemophilus
8	7	5.1	118	1 RL19_BACSU	Q31742 bacillus su
9	7	5.1	175	1 MP54_PHAHQ	P56167 phalaris aq
10	7	5.1	183	1 RBS_AMAHP	Q42516 amaranthus
11	7	5.1	195	1 VP12_BPPH6	P07580 bacterioph
12	7	5.1	308	1 MP5A_LOLPR	Q40240 lolium pere
13	7	5.1	320	1 MP51_PHAHQ	P56164 phalaris aq
14	7	5.1	333	1 MP92_POAPR	P22285 poa pratens
15	7	5.1	351	1 Y887_MEPTH	Q26973 methanobact
16	7	5.1	378	1 PEM1_PHACH	Q02567 phanerocha
17	7	5.1	418	1 DFP_MYCTU	P71661 mycobacteri
18	7	5.1	421	1 CLPX_CHLPN	Q92760 chlamydia p
19	7	5.1	485	1 NMTB_ECOLI	P32154 escherichia
20	7	5.1	498	1 NWT2_HUMAN	Q06551 homo sapien
21	7	5.1	568	1 ZRF1_HUMAN	Q99543 homo sapien
22	7	5.1	610	1 YH98_MYCTU	Q53947 mycobacteri
23	7	5.1	793	1 CALD_HUMAN	Q05682 homo sapien
24	7	5.1	807	1 OXYB_HUMAN	P22059 homo sapien
25	7	5.1	809	1 OXYB_RABIT	P16258 oryctolagus
26	7	5.1	1329	1 FTSK_ECOLI	P46889 escherichia
27	7	5.1	1842	1 FAS2_SCHPO	Q10289 schizosacch
28	6	4.3	67	1 YPHE_BACSU	P50744 bacillus su
29	6	4.3	73	1 Y055_NPVAC	P41459 autographa
30	6	4.3	100	1 YG10_HSVEB	P28980 equine herp
31	6	4.3	103	1 MGP_HUMAN	P08493 homo sapien
32	6	4.3	103	1 MGP_RABIT	P47841 oryctolagus
33	6	4.3	103	1 MGP_RAT	P08494 rattus norv

ALIGNMENTS

RESULT 1

ID	MPP6_PHLPR	STANDARD	PRT	132 AA
AC	P43215;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	POLLEN ALLERGEN PHL P 6 PRECURSOR (PHL P VI).			
GN	PHLPVI.			
OS	Phleum pratense (Common timothy).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Pooeae; Phleum.			
OX	NCBI_TaxID=15957;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. AGROSTIDEAE 24W28-7C;			
RX	MEDLINE=95375564; PubMed=7647586;			
RA	Petersen A., Bufe A., Schramm G., Schlaak M., Becker W.;			
RT	"Characterization of the allergen group VI in timothy grass pollen to (PHL P 6). II. cDNA cloning of PHL P 6 and structural comparison to grass group V.";			
RL	Grass Allergy: Immunol. 108:55-59(1995).			
CC	!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.			
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CC	EMBL; Z27082; CAA81608.1; -			
DR	InterPro; IPR002914; -			
DR	Pfam; PF01620; Pollen_allerg_2; 1.			
KW	Allergen; Signal.			
FT	SIGNAL 1 22 POTENTIAL..			
FT	CHAIN 23 132 POLLEN ALLERGEN PHL P 6.			
SQ	SEQUENCE 132 AA; 13921 MW; 3513D3D85069D5F8 CRC64;			
Query Match 58.0%; Score 80; DB 1; Length 132;				
Best Local Similarity 100.0%; Pred. No. 3.9e-74;				
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	43 NASFRAMATTANVPADKYKTFEAAFTVSSKRNLADAVSKAPQOLVPKLDDEVNAAYNAA 102			
Db				
Oy	37 NASFRAMATTANVPADKYKTFEAAFTVSSKRNLADAVSKAPQOLVPKLDDEVNAAYNAA 96			
Oy	103 DHAAPEDKYEAFVLHFSEAL 122			

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Db 97 DHAAPDKYAEVLFSEAL 116
RESULT 2
MP5B_PHLPR STANDARD; PRT; 284 AA.
ID Q40963;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE POLLEN ALLERGEN PHL P 5B PRECURSOR (PHL P VB) (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AGROSTIDEAE; TISSUE=Pollen;
RX MEDLINE=95246885; PubMed=7729355;
RA Bufo A., Schramm G., Keown M.B., Schlaak M., Becker W.M.;
RT "Major allergen PHL p Vb in timothy grass is a novel pollen RNase.";
RL FEBS Lett. 363:6-12(1995).
RN [2]
RP REVISIONS.
RA Bufo A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HAS RIBONUCLEASE ACTIVITY. MAY BE INVOLVED IN HOST-
CC PATHOGEN INTERACTIONS.
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z27083; CAA81609.1; -
CC InterPro: IPR002914; -
CC Pfam: PF01620; Pollen_allerg.2; 1.
CC Signal; Allergen.
CC NON_TER 1
CC CHAIN <1 19 POTENTIAL.
CC SIGNAL 20 284 POLLEN ALLERGEN PHL P 5B.
CC SEQUENCE 284 AA; 28001 MW; E949FB3E0985295E CRC64;
Query Match 10.9%; Score 15; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 9,1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GKATTEQKLIEDIN 43
Db 37 GKATTEQKLIEDIN 51
RESULT 3
MP5A_PHLPR STANDARD; PRT; 286 AA.
ID Q40962;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE POLLEN ALLERGEN PHL P 5A (PHL P VA) (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AGROSTIDEAE;
RX MEDLINE=94085783; PubMed=8262382;
RA Ong E.K., Griffith I.J., Knox R.B., Singh M.B.;
RT "Cloning of a cDNA encoding a group-V (group-IX) allergen isoform
RT from rye-grass pollen that demonstrates specific antigenic
RT immunoreactivity.";
RL Gene 134:235-240(1993).
CC -!- SUBCELLULAR LOCATION: STARCH GRANULE (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: POLLEN, STARCH GRANULES (BY SIMILARITY).
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
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CC -----
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RX MEDLINE=94342654; PubMed=7520460;
RA Bufo A., Becker W.M., Schramm G., Petersen A., Mamat U., Schlaak M.;
RT "Major allergen PHL p Va (timothy grass) bears at least two different
RT IGE-reactive epitopes.";
RL J. Allergy Clin. Immunol. 94:173-181(1994).
RN [2]
RP REVISIONS.
RA Bufo A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EXPORT PROTEIN.
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X70942; CAA50281.1; -
CC HSSP: P04002; IWFA
CC InterPro: IPR002914; -
CC Pfam: PF01620; Pollen_allerg.2; 1.
CC NON_TER 1
CC SEQUENCE 286 AA; 28530 MW; COE12BE83A3070F5 CRC64;
Query Match 8.7%; Score 12; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GKATTEQKLE 40
Db 32 GKATTEQKLE 43
RESULT 4
MP5B_LOLPR STANDARD; PRT; 339 AA.
ID Q40237;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MAJOR POLLEN ALLERGEN LOL P 5B PRECURSOR (LOL P VB).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=94085783; PubMed=8262382;
RA Ong E.K., Griffith I.J., Knox R.B., Singh M.B.;
RT "Cloning of a cDNA encoding a group-V (group-IX) allergen isoform
RT from rye-grass pollen that demonstrates specific antigenic
RT immunoreactivity.";
RL Gene 134:235-240(1993).
CC -!- SUBCELLULAR LOCATION: STARCH GRANULE (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: POLLEN, STARCH GRANULES (BY SIMILARITY).
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
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DR EMBL: L13083; AAA33405.1; -.
DR HSSP: P04002; IWFA.
DR InterPro: IPR001778; -.
DR Pfam: PF01620; Pollen.allerg.2; 1.
DR PRINTS: PR00833; POAALLERGEN.
KW Signal; Allergen; Multigene family; Repeat.
FT SIGNAL 1 25
FT CHAIN 26 339
FT DOMAIN 32 58 MAJOR POLLEN ALLERGEN LOL P 5B.
FT REPEAT 32 58 9 X 3 AA TANDEM REPEATS OF [PA]-A-[TA].
FT REPEAT 32 58 1-1.
FT REPEAT 32 58 1-2.
FT REPEAT 35 37 1-1.
FT REPEAT 35 37 1-2.
FT REPEAT 38 40 1-3.
FT REPEAT 41 43 1-3.
FT REPEAT 41 43 1-4.
FT REPEAT 44 46 1-5.
FT REPEAT 47 49 1-6.
FT REPEAT 50 52 1-7.
FT REPEAT 53 55 1-8.
FT REPEAT 56 58 1-9.
FT DOMAIN 285 334 6 X 9 AA APPROXIMATE TANDEM REPEATS OF
T-A-T-A-T-P-A-A-A.
FT REPEAT 285 290 2-1 (INCOMPLETE).
FT REPEAT 292 300 2-2.
FT REPEAT 301 309 2-3.
FT REPEAT 310 318 2-4.
FT REPEAT 319 327 2-5.
FT REPEAT 328 334 2-6 (INCOMPLETE).
FT DOMAIN 81 87 POLY-ALA.
FT DOMAIN 288 293 POLY-ALA.
SQ SEQUENCE 339 AA; 33750 MW; 3CAA3115625E0610 CRC64;

Query Match 8.7%; Score 12; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEOKLIE 40
Db 62 GKATTEOKLIE 73

RESULT 5
MP53_PHAHQ STANDARD; PRT; 294 AA.
AC P56166;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MAJOR POLLEN ALLERGEN PHA A 5.3 PRECURSOR (PHA A 5) (CLONE 29).
OS Phalaris aquatica (Canary grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Poaceae; Poaceae;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Phalaris.
OX NCBI_TaxID=28479;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=96105569; PubMed=8564724;
RA Suphioglu C., Singh M.B.;
RT "Cloning, sequencing and expression in Escherichia coli of Pha a 1
and four isoforms of Pha a 5, the major allergens of canary grass
pollen.";
RL Clin. Exp. Allergy 25:853-865(1995).
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
DR InterPro: IPR002914; -.
DR Pfam: PF01620; Pollen.allerg.2; 1.
KW Allergen; Multigene family; Signal.
FT SIGNAL 1 25
FT CHAIN 26 294 MAJOR POLLEN ALLERGEN PHA A 5.3.
SQ SEQUENCE 294 AA; 30344 MW; 9DFC541079C1CC00 CRC64;

EMBL: L13083; AAA33405.1; -.
HSSP: P04002; IWFA.
InterPro: IPR001778; -.
Pfam: PF01620; Pollen.allerg.2; 1.
PRINTS: PR00833; POAALLERGEN.
Signal; Allergen; Multigene family; Repeat.
SIGNAL 1 25
CHAIN 26 339
DOMAIN 32 58 MAJOR POLLEN ALLERGEN LOL P 5B.
REPEAT 32 58 9 X 3 AA TANDEM REPEATS OF [PA]-A-[TA].
REPEAT 32 58 1-1.
REPEAT 32 58 1-2.
REPEAT 35 37 1-1.
REPEAT 35 37 1-2.
REPEAT 38 40 1-3.
REPEAT 41 43 1-3.
REPEAT 41 43 1-4.
REPEAT 44 46 1-5.
REPEAT 47 49 1-6.
REPEAT 50 52 1-7.
REPEAT 53 55 1-8.
REPEAT 56 58 1-9.
DOMAIN 285 334 6 X 9 AA APPROXIMATE TANDEM REPEATS OF
T-A-T-A-T-P-A-A-A.
REPEAT 285 290 2-1 (INCOMPLETE).
REPEAT 292 300 2-2.
REPEAT 301 309 2-3.
REPEAT 310 318 2-4.
REPEAT 319 327 2-5.
REPEAT 328 334 2-6 (INCOMPLETE).
DOMAIN 81 87 POLY-ALA.
DOMAIN 288 293 POLY-ALA.
SEQUENCE 339 AA; 33750 MW; 3CAA3115625E0610 CRC64;

Query Match 8.7%; Score 12; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEOKLIE 40
Db 62 GKATTEOKLIE 73

RESULT 5
MP53_PHAHQ STANDARD; PRT; 294 AA.
AC P56166;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MAJOR POLLEN ALLERGEN PHA A 5.3 PRECURSOR (PHA A 5) (CLONE 29).
OS Phalaris aquatica (Canary grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Poaceae; Poaceae;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Phalaris.
OX NCBI_TaxID=28479;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=96105569; PubMed=8564724;
RA Suphioglu C., Singh M.B.;
RT "Cloning, sequencing and expression in Escherichia coli of Pha a 1
and four isoforms of Pha a 5, the major allergens of canary grass
pollen.";
RL Clin. Exp. Allergy 25:853-865(1995).
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
DR InterPro: IPR002914; -.
DR Pfam: PF01620; Pollen.allerg.2; 1.
KW Allergen; Multigene family; Signal.
FT SIGNAL 1 25
FT CHAIN 26 294 MAJOR POLLEN ALLERGEN PHA A 5.3.
SQ SEQUENCE 294 AA; 30344 MW; 9DFC541079C1CC00 CRC64;
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Query Match 7.2%; Score 10; DB 1; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 EOKLIEDINA 44
Db 51 EOKLIEDINA 60

RESULT 6
NU3M_STRPU STANDARD; PRT; 116 AA.
ID NU3M_STRPU
AC P15550;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
GN ND3.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OS Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89011951; PubMed=3172215;
RA Jacobs H.T., Elliott D.J., Math V.B., Farquharson A.;
RT "Nucleotide sequence and gene organization of sea urchin
mitochondrial DNA.";
RL J. Mol. Biol. 202:185-217(1988).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
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CC EMBL: X12631; CAA31158.1; -.
DR PIR: S01507; S01507.
DR InterPro: IPR000440; -.
DR Pfam: PF00507; oxidored_q4; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 116 AA; 12734 MW; CF507E95FB772204 CRC64;

Query Match 6.5%; Score 9; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVAVVLGLA 21
Db 13 AVAVVLGLA 21

RESULT 7
YG81_HAEIN STANDARD; PRT; 221 AA.
ID YG81_HAEIN
AC P44290;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL PROTEIN HI1681 PRECURSOR.
GN HI1681
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT Influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- SIMILARITY: TO E.COLI YCCT.
CC -----
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CC -----
CC EMBL; U32841; AAC23327.1; -;
DR TIGR; H11681; -;
KW Hypothetical protein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 221 HYPOTHETICAL PROTEIN H11681.
SQ SEQUENCE 221 AA; 23395 MW; D30BBEAC9C0E03C6 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AVVLGLAT 22
Db 5 AVVLGLAT 12

RESULT 8
RL19_BACSU STANDARD; PRT; 118 AA.
ID RL19_BACSU
AC Q31742;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 50S RIBOSOMAL PROTEIN L19.
GN RPLS.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SUBUNIT
CC INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE
CC AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----

DR EMBL; Z99112; CAB13477.1; -;
DR Subtilist; BG12667; rpls.
DR InterPro; IPR001857; -;
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMAL_L19.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Ribosomal protein.
SQ SEQUENCE 118 AA; 13747 MW; 31E57C82256D0A70 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QKLIEDI 42
Db 5 QKLIEDI 11

RESULT 9
MP54_PHAHQ STANDARD; PRT; 175 AA.
ID MP54_PHAHQ
AC P56167;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE MAJOR POLLEN ALLERGEN PHA A 5.4 (PHA A 5) (CLONE 5) (FRAGMENT).
OS Phalaris aquatica (Canary grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Poaceae;
OC Phalaris.
OX NCBI_TaxID=28479;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Pollen;
RX MEDLINE=96105569; PubMed=8564724;
RA Suphioglu C., Singh M.B.;
RT "Cloning, sequencing and expression in Escherichia coli of Pha a 1
RT and four isoforms of Pha a 5, the major allergens of canary grass
RT pollen.";
RL Clin. Exp. Allergy 25:853-865(1995).
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
KW Allergen; Multigene family.
FT NON_TER 1
SQ SEQUENCE 175 AA; 17860 MW; 450B07C306CAAC6C CRC64;

Query Match 5.1%; Score 7; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
Db 22 EVHAVKP 28

RESULT 10
RBS_AMAHP STANDARD; PRT; 183 AA.
ID RBS_AMAHP
AC Q42516;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39)
DE (RUBISCO SMALL SUBUNIT).
GN RBS.
OS Amaranthus hypochondriacus (Prince's feather).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC Caryophyllales; Amaranthaceae; Amaranthus.
OX NCBI_TaxID=28502;
RN [1]

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DR EMBL; M12921; AAA32359.1; -.
DR PIR; B23368; YHPPF6.
SQ SEQUENCE 195 AA; 20293 MW; 460727BED818F60B CRC64;

Query Match 5.1%; Score 7; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVAVVLG 19
|||||||
Db 44 AVAVVLG 50
|||||||

RESULT 12
MP5A_LOLPR STANDARD; PRT; 308 AA.

AC Q40240;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MAJOR POLLEN ALLERGEN LOL P 5A PRECURSOR (LOL P VA) (LOL P IB).
GN LOL PRB.
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poeae; Lolium.
NCBI_TaxID=4522;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91142177; PubMed=1671715;
RA Singh M.B., Hought T., Theerakulpisit P., Avjoglou A., Davies S.,
RA Smith P.M., Taylor P., Simpson R.J., Ward L.D., McCluskey J.,
PU Puy R., Knox R.B.;
RT Isolation of cDNA encoding a newly identified major allergenic protein of rye-grass pollen: intracellular targeting to the amyloplast.
RL Proc. Natl. Acad. Sci. U.S.A. 88:1384-1388(1991).
CC -!- SUBCELLULAR LOCATION: STARCH GRANULE.
CC -!- TISSUE SPECIFICITY: POLLEN, STARCH GRANULES.
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.

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DR EMBL; M59163; AAA33406.1; -.
DR InterPro; IPR002914; -.
DR Pfam; PF01620; Pollen.allerg.2; 1.
KW Signal; Allergen; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 308 MAJOR POLLEN ALLERGEN LOL P 5A.
FT DOMAIN 31 46 ALA/PRO/THR-RICH.
FT DOMAIN 270 289 ALA/THR-RICH.
FT DOMAIN 33 36 POLY-ALA.
FT DOMAIN 270 278 POLY-ALA.
SQ SEQUENCE 308 AA; 31881 MW; 7756025D09E12FFF CRC64;

Query Match 5.1%; Score 7; DB 1; Length 308;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 EVHAVKP 136

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Db 151 EVHAVKP 157
|||||||
RESULT 13
MP51_PHAHQ
ID MP51_PHAHQ STANDARD; PRT; 320 AA.
AC P56164;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MAJOR POLLEN ALLERGEN PHA A 5.1 PRECURSOR (PHA A 5) (CLONE 28).
OS Phalaris aquatica (Canary grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poaceae;
OC Phalaris.
OX NCBI_TaxID=28479;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RA MEDLINE=96105569; PubMed=8564724;
RA Suphioglu C., Singh M.B.;
RT "Cloning, sequencing and expression in Escherichia coli of Pha a 1
RT and four isoforms of Pha a 5, the major allergens of canary grass
RT pollen.";
RL Clin. Exp. Allergy 25:853-865(1995).
CC -!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
DR InterPro: IPR002914;
DR Pfam: PF01620; Pollen_allerg_2; 1.
KW Allergen; Multigene family; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 320 MAJOR POLLEN ALLERGEN PHA A 5.1.
SQ SEQUENCE 320 AA; 33548 MW; 683BC6AEC37EED29 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||||
Db 139 EVHAVKP 145

RESULT 14
MP92_POAPR
ID MP92_POAPR STANDARD; PRT; 333 AA.
AC P22285;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE POLLEN ALLERGEN KEG 41 PRECURSOR (POLLEN ALLERGEN POA P 9) (POA P IX).
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RA MEDLINE=91093322; PubMed=1702432;
RA Silvanovich A., Astwood J., Zhang L., Olsen E., Kisil F.T.,
RA Sehon A.H., Mohapatra S.S., Hill R.D.;
RT "Nucleotide sequence analysis of three cDNAs coding for Poa p IX
RT isoallergens of Kentucky bluegrass pollen.";
RL J. Biol. Chem. 266:1204-1210(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=91268549; PubMed=2051020;
RA Olsen E., Zhang L., Hill R.D., Kisil F.T., Sehon A.H., Mohapatra S.S.;
RT "Identification and characterization of the Poa p IX group of basic
RT allergens of Kentucky bluegrass pollen.";
RL J. Immunol. 147:205-211(1991).

-!- TISSUE SPECIFICITY: POLLEN.
-!- MISCELLANEOUS: ITS C-TERMINUS MIGHT BE MEMBRANE-ASSOCIATED.
-!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
-----
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-----
CC EMBL; M38343; AAA63456.1;
CC PIR; A39098; A39098.
CC InterPro: IPR001778;
CC InterPro: IPR002914;
CC Pfam: PF01620; Pollen_allerg_2; 1.
CC PRINTS; PR00833; POALLERGEN.
KW Allergen; Signal; Multigene family; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 333 POLLEN ALLERGEN KEG 41.
FT DOMAIN 309 332 2 X 12 AA TANDEM REPEATS.
FT REPEAT 309 320 1.
FT REPEAT 321 332 2.
SQ SEQUENCE 333 AA; 32661 MW; 1FA48168C1134CA0 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||||
Db 170 EVHAVKP 176

RESULT 15
Y887_METTH
ID Y887_METTH STANDARD; PRT; 351 AA.
AC O26973;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL PROTEIN MTH887.
GN MTH887.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RA MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE UPF0104 FAMILY.
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CC EMBL: AE000864; AAB85385.1; -
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 51 71 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 165 185 POTENTIAL.
FT TRANSMEM 244 264 POTENTIAL.
FT TRANSMEM 275 295 POTENTIAL.
FT TRANSMEM 304 324 POTENTIAL.
FT TRANSMEM 328 348 POTENTIAL.
SQ SEQUENCE 351 AA; 38628 MW; 37AD5210A93A4716 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FLAVAVV 17
| | | | | | |
DB 24 FLAVAVV 30

RESULT 16
PEMI_PHACH STANDARD; PRT; 378 AA.
AC Q02567; Q01788;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PEROXIDASE MANGANESE-DEPENDENT I PRECURSOR (EC 1.11.1.7) (MNP-1)
DE (MNP1) (MANGANESE PEROXIDASE ISOZYME 1).
GN MNP1.
OS Phanerochaete chrysosporium.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Stereales;
OC Corticiaceae; Phanerochaete.
OX NCBI_TaxID=5306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OGC101;
RX MEDLINE=91033001; PubMed=2227420;
RA Godfrey B.J., Mayfield M.B., Brown J.A., Gold M.H.;
RT "Characterization of a gene encoding a manganese peroxidase from
Phanerochaete chrysosporium.";
RL Gene 93:119-124(1990).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-41.
RC STRAIN=OGC101;
RX MEDLINE=89174785; PubMed=2925681;
RA Pribnow D., Mayfield M.B., Nipper V.J., Brown J.A., Gold M.H.;
RT "Characterization of a cDNA encoding a manganese peroxidase, from the
lignin-degrading basidiomycete Phanerochaete chrysosporium.";
RL J. Biol. Chem. 264:5036-5040(1989).
RN [3]
RP METAL-BINDING.
RX MEDLINE=96280658; PubMed=8688436;
RA Kishi K., Kusters-van Someren M., Mayfield M.B., Sun J., Loefer T.M.,
RA Gold M.H.;
RT "Characterization of manganese(II) binding site mutants of manganese
peroxidase.";
RL Biochemistry 35:8986-8994(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS).
RX MEDLINE=95105154; PubMed=7806497;
RA Sundaramoorthy M., Kishi K., Gold M.H., Poulos T.L.;
RT "The crystal structure of manganese peroxidase from Phanerochaete
chrysosporium at 2.06-A resolution.";
RL J. Biol. Chem. 269:32759-32767(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MUTANTS.
RX MEDLINE=97362247; PubMed=9211904;
RA Sundaramoorthy M., Kishi K., Gold M.H., Poulos T.L.;
RT "Crystal structures of substrate binding site mutants of manganese
```

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peroxidase.";
J. Biol. Chem. 272:17574-17580(1997).
CC -!- FUNCTION: CATALYZES THE OXIDATION OF MN(II) TO MN(III). THE
LATTER, ACTING AS A DIFFUSIBLE REDOX MEDIATOR, IS CAPABLE OF
OXIDIZING A VARIETY OF LIGNIN COMPOUNDS.
CC -!- CATALYTIC ACTIVITY: 2 MN(II) + 2 H(+) + H(2)O(2) = 2 MN(III) + 2
H(2)O.
CC -!- COFACTOR: BINDS HEME.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- INDUCTION: DURING WOUND-HEALING AND BY FACTORS WHICH INDUCE
SUBERIZATION.
CC -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. LIGNINASE SUBFAMILY.
CC
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CC
DR EMBL: M60672; AAA33744.1; -
DR EMBL: M77513; AAA33743.1; -
DR EMBL: J04624; AAA33742.1; -
DR PIR: JN0092; JN0092.
DR PDB: 1MN1; 04-SEP-97.
DR PDB: 1MN2; 04-SEP-97.
DR PDB: 1MNP; 15-SEP-95.
DR InterPro: IPR001621; -
DR InterPro: IPR002016; -
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE.
DR PRINTS: PR00462; LIGNINASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;
Lignin degradation; Metal-binding; Manganese; Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 378 PEROXIDASE MANGANESE-DEPENDENT I.
FT ACT_SITE 63 63 DISTAL ARGININE (BY SIMILARITY).
FT ACT_SITE 67 67 DISTAL HISTIDINE (BY SIMILARITY).
FT ACT_SITE 194 194 PROXIMAL HISTIDINE (HEME AXIAL LIGAND).
FT METAL 56 56 MANGANESE.
FT METAL 60 60 MANGANESE.
FT METAL 200 200 MANGANESE.
FT DISULFID 24 36
FT DISULFID 35 310
FT DISULFID 54 138
FT DISULFID 274 340
FT DISULFID 362 369
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 75 75 S -> L (IN REF. 2).
SQ SEQUENCE 378 AA; 39556 MW; 17A9A8F642441F27 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 ASFRAAM 50
| | | | | | |
DB 288 ASFRAAM 294

RESULT 17
DEFP_MYCTU STANDARD; PRT; 418 AA.
ID DEFP_MYCTU
AC P71661;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
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DE DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.
GN DFP OR RV1391 OR MTC21B4.08.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Church C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies T., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -!- FUNCTION: FLAVOPROTEIN AFFECTING SYNTHESIS OF DNA AND PANTOTHENATE
CC METABOLISM (BY SIMILARITY).
CC -----
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CC -----
CC EMBL: Z80108; CAB02174.1; -;
DR Tuberculist; Rv1391; -;
KW Flavoprotein.
SQ SEQUENCE 418 AA; 43577 MW; 48BD95E536595506 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 LADAVSK 83
Db 263 LADAVSK 269

RESULT 18
CLPX_CHLPN
ID CLPX_CHLPN STANDARD; PRT; 421 AA.
AC Q92760; Q9JQE4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX.
GN CLPX OR CPN0846 OR CPl023.
OS Chlamydia pneumoniae (Chlamydiales; Chlamydiaceae; Chlamydia).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hiçkey E.K., Peterson J., Utterback T., Berry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- FUNCTION: ATP-DEPENDENT SPECIFICITY COMPONENT OF THE CLP PROTEASE.
CC IT DIRECTS THE PROTEASE TO SPECIFIC SUBSTRATES. CAN PERFORM
CC CHAPERONE FUNCTIONS IN THE ABSENCE OF CLPP (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF CLPP AND CLPX (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY.
CC -----
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CC -----
CC EMBL: AE001665; AAD18984.1; -;
DR EMBL: AE002259; AAF38799.1; -;
DR EMBL: AP002548; BAA99054.1; -;
DR TIGR; CPl023; -;
DR InterPro; IPR001270; -;
DR InterPro; IPR001939; -;
DR Pfam; PF00004; AAA; 1;
DR PRINTS; PR00300; CLPPPROTEASEA.
KW Chaperone; ATP-binding.
FT ZN_FING 9 34 C4-TYPE.
FT NP_BIND 122 129 ATP (POTENTIAL).
FT SEQUENCE 421 AA; 46351 MW; BEFB6BECE3B007F3 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TTANVPP 58
Db 221 TTANVPP 227

RESULT 19
PTVB_ECOLI
ID PTVB_ECOLI STANDARD; PRT; 485 AA.
AC P32154;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PTS SYSTEM, FRUCTOSE-LIKE-1 IIIC COMPONENT (PHOSPHOTRANSFERASE ENZYME
DE II, BC COMPONENT) (EC 2.7.1.69).
GN FRVB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93347969; PubMed=8346018;
RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";

RL Nucleic Acids Res. 21:3391-3398(1993).
RN [2]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=94290319; PubMed=8019415;
RA Reizer J., Michotey V., Reizer A., Saier M.H. Jr.;
RT "Novel phosphotransferase system genes revealed by bacterial genome
RT analysis; unique, putative fructose- and glucoside-specific
RT systems.";
RL Protein Sci. 3:440-450(1994).
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
CC -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
CC AND THE TRANSMEMBRANE CHANNEL. THE IIA DOMAIN CONTAINS THE PRIMARY
CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
CC THE SUGAR.
CC -!- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
CC PROTEIN HISTIDINE + SUGAR PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
CC -!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
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CC -----
CC EMBL; L19201; AB03032.1; -
CC EMBL; AE000465; AAC76881.1; -
CC PIR; S40843; S40843.
CC EcoGene; EG11863; frvB.
KW Phosphotransferase system; Sugar transport; Transferase;
KW Transmembrane; Inner membrane; Phosphorylation.
FT DOMAIN 1 ? EIIB DOMAIN.
FT DOMAIN ? 485 EIIC DOMAIN.
FT MOD_RES 15 15 PHOSPHORYLATION (POTENTIAL).
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 182 202 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 266 286 POTENTIAL.
FT TRANSMEM 305 325 POTENTIAL.
FT TRANSMEM 346 366 POTENTIAL.
FT TRANSMEM 382 402 POTENTIAL.
FT TRANSMEM 404 424 POTENTIAL.
FT TRANSMEM 444 464 POTENTIAL.
SQ SEQUENCE 485 AA; 51322 MW; E6D2FA72730C2B87 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AVVLGLA 21
Db 235 AVVLGLA 241
| | | | |
| | | | |

RESULT 20
ZRF1_HUMAN
ID NMT2_HUMAN STANDARD; PRT; 498 AA.
AC O60551;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE 2 (EC 2.3.1.97) (PEPTIDE N-
DE MYRISTOYLTRANSFERASE 2) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE
DE 2) (NMT 2).

GN NMT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98175914; PubMed=9506952;
RA Giang D.K., Cravatt B.F.;
RT "A second mammalian N-myristoyltransferase.";
RL J. Biol. Chem. 273:6595-6598(1998).
CC -!- FUNCTION: ADDS MYRISTOYL GROUP TO N-TERMINAL GLYCINE RESIDUE OF
CC CERTAIN CELLULAR AND VIRAL PROTEINS.
CC -!- CATALYTIC ACTIVITY: TETRADECANOYL-COA + GLYCYL-PEPTIDE = COA + N-
CC TETRADECANOYLGLYCYL-PEPTIDE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.
CC -----
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CC -----
CC EMBL; AF043325; AAC09295.1; -
CC MIM; 603801; -
CC InterPro; IPR000903; -
CC Pfam; PF01233; NMT; 1.
CC PROSITE; PS00975; NMT_1; 1.
CC PROSITE; PS00976; NMT_2; 1.
KW Transferase; Acyltransferase. POLY-LYS.
FT DOMAIN 46 56
SQ SEQUENCE 498 AA; 56980 MW; 1B1486CC6559B6A9 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 VPKLDEV 94
Db 127 VPKLDEV 133
| | | | |
| | | | |

RESULT 21
ZRF1_HUMAN
ID ZRF1_HUMAN STANDARD; PRT; 568 AA.
AC Q99543;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ZUOTIN RELATED FACTOR-1 (M-PHASE PHOSPHOPROTEIN 11).
GN ZRF1 OR MPOSPH11 OR MPPL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97039687; PubMed=8885239;
RA Matsumoto-Taniura N., Pirolet F., Monroe R., Gerace L.,
RA Westendorf J.M.;
RT "Identification of novel M phase phosphoproteins by expression
RT cloning.";
RL Mol. Biol. Cell 7:1455-1469(1996).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED IN M (MITOTIC) PHASE.
CC -!- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -----

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DR EMBL; X98260; CAA66913.1; ALT_INIT.
DR MIM; G05502; -
DR HSSP; P25685; 1HDJ.
DR InterPro: IPR001005; -
DR InterPro: IPR001623; -
DR Pfam; PF00226; DnaJ; 1.
DR PROSITE; PS00249; myb_DNA-binding; 2.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PROSITE; PS00076; DNAJ_2; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 1.
DR Chapterone; Nuclear protein; Phosphorylation.
KW DOMAIN 94 163 J-DOMAIN.
FT SEQUENCE 568 AA; 65913 MW; 32F269BA4532AD46 CRC64;
SQ

Query Match 5.1%; Score 7; DB 1; Length 568;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTEEQKL 38
| | | | |
DB 502 TTEEQKL 508

RESULT 22
YH98_MYCTU
ID YH98_MYCTU STANDARD; PRT; 610 AA.
AC 053947;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOPHENICAL 67.8 KDA PROTEIN RV1798.
GN RV1798 OR MTV049.20.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).

CC -1- SIMILARITY: BELONGS TO THE CBXX/CFOX FAMILY.
CC
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DR EMBL; AL022021; CAA17719.1; -
DR TubercuList; RV1798; -

DR InterPro: IPR001939; -
DR Pfam; PF00004; AAA; 1.
KW Hypothetical protein; ATP-binding.
FT NP_BIND 357 364 ATP (POTENTIAL).
SQ SEQUENCE 610 AA; 67755 MW; E6DE3C2D1C5356BC CRC64;

Query Match 5.1%; Score 7; DB 1; Length 610;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 AAMATTA 54
| | | | |
DB 186 AAMATTA 192

RESULT 23
CALD_HUMAN
ID CALD_HUMAN STANDARD; PRT; 793 AA.
AC Q05682; Q13979; Q13978; Q14741; Q14742;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CALDESMON (CDM).
GN CALDI OR CDM OR CAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM WI-38 L-CAD II).
RX TISSUE=Lung fibroblast;
RX MEDLINE=91358497; PubMed=1885618;
RA Novy R.E., Lin J.L.-C., Lin J.J.-C.;
RT "Characterization of cDNA clones encoding a human fibroblast
RT caldesmon isoform and analysis of caldesmon expression in normal and
RT transformed cells.";
RL J. Biol. Chem. 266:16917-16924(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS WI-38 L-CAD II AND H-CAD).
RX TISSUE=Aorta;
RX MEDLINE=92209999; PubMed=1555769;
RA Humphrey M.B., Herrera-Sosa H., Gonzalez G., Lee R., Bryan J.;
RT "Cloning of cDNAs encoding human caldesmons.";
RL Gene 112:197-204(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS HELA L-CAD I AND II).
RX MEDLINE=93101679; PubMed=1465449;
RA Hayashi K., Yano H., Hashida T., Takeuchi R., Takeda O., Asada K.,
RA Takahashi E.-I., Kato I., Sobue K.;
RT "Genomic structure of the human caldesmon gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:12122-12126(1992).
CC -1- FUNCTION: ACTIN- AND MYOSIN-BINDING PROTEIN IMPLICATED IN THE
CC REGULATION OF ACTOMYOSIN INTERACTIONS IN SMOOTH MUSCLE AND
CC NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN AND ACTIN
CC FILAMENTS). STIMULATES ACTIN BINDING OF TROPOMYOSIN WHICH
CC INCREASES THE STABILIZATION OF ACTIN FILAMENT STRUCTURE. IN MUSCLE
CC TISSUES, INHIBITS THE ACTOMYOSIN ATPASE BY BINDING TO F-ACTIN.
CC THIS INHIBITION IS ATTENUATED BY CALCIUM-CALMODULIN AND IS
CC POTENTIATED BY TROPOMYOSIN. INTERACTS WITH ACTIN, MYOSIN, TWO
CC MOLECULES OF TROPOMYOSIN AND WITH CALMODULIN. ALSO PLAY AN
CC ESSENTIAL ROLE DURING CELLULAR MITOSIS AND RECEPTOR CAPPING.
CC -1- SUBCELLULAR LOCATION: ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON
CC STRESS FIBERS IN FIBROBLASTS (NONMUSCLE) (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: THREE NON-MUSCLE ISOFORMS CALLED HELA L-CAD
CC I, HELA L-CAD II, WI-38 L-CAD I, WI-38 L-CAD II/1-CAD AND ONE
CC SMOOTH-MUSCLE ISOFORM H-CAD (SHOWN HERE) ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGH-MOLECULAR-WEIGHT CALDESMON (H-CALDESMON)
CC IS PREDOMINANTLY EXPRESSED IN SMOOTH MUSCLES, WHEREAS LOW-
CC MOLECULAR-WEIGHT CALDESMON (L-CALDESMON) IS WIDELY DISTRIBUTED IN
CC NON-MUSCLE TISSUES AND CELLS. NOT EXPRESSED IN SKELETAL MUSCLE OR
CC HEART.

CC -!- DOMAIN: THE N-TERMINAL PART SEEMS TO BE A MYOSIN/CALMODULIN-
CC BINDING DOMAIN, AND THE C-TERMINAL A TROPOMYOSIN/ACTIN/CALMODULIN-
CC HELICAL REGION IN THE SMOOTH-MUSCLE FORM.
CC -!- PTM: IN NON-MUSCLE CELLS, PHOSPHORYLATION BY CDC2 DURING MITOSIS
CC CAUSES CALDESMON TO DISSOCIATE FROM MICROFILAMENTS.
CC PHOSPHORYLATION REDUCES CALDESMON BINDING TO ACTIN, MYOSIN, AND
CC CALMODULIN AS WELL AS ITS INHIBITION OF ACTOMYOSIN ATPASE
CC ACTIVITY. PHOSPHORYLATION ALSO OCCURS IN BOTH QUIESCENT AND
CC DIVIDING SMOOTH MUSCLE CELLS WITH SIMILAR EFFECTS ON THE
CC INTERACTION WITH ACTIN AND CALMODULIN AND ON MICROFILAMENTS
CC REORGANIZATION (BY SIMILARITY).
CC -!- SIMILARITY: TO A TROPOMYOSIN BINDING SITE DOMAIN OF TROPONIN T.
CC -----
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CC -----
DR EMBL; M64110; AAA35636.1; -
DR EMBL; M83216; AAA58420.1; -
DR EMBL; M83216; AAA58419.1; -
DR EMBL; D90452; BAA14418.1; -
DR EMBL; D90453; BAA14419.1; -
DR MIM; I14213; -
DR InterPro; IPR000075; -
DR Pfam; PF02029; Caldesmon; 1.
DR PRINTS; PR01076; CALDESMON.
DR Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
KW Repeat; Alternative splicing.
FT FT 319 375
FT FT 319 332
FT REPEAT 333 346
FT REPEAT 347 360
FT DOMAIN 26 207
FT FT MYOSIN AND CALMODULIN-BINDING (BY
FT SIMILARITY).
FT DOMAIN 564 621
FT DOMAIN 664 674
FT DOMAIN 653 686
FT DOMAIN 716 722
FT DOMAIN 768 793
FT DOMAIN 39 46
FT DOMAIN 81 86
FT DOMAIN 189 196
FT DOMAIN 376 379
FT DOMAIN 540 543
FT DOMAIN 580 583
FT DOMAIN 597 600
FT MOD_RES 724 724
FT FT PHOSPHORYLATION (BY CDC2) (BY
FT SIMILARITY).
FT FT 730 730
FT FT PHOSPHORYLATION (BY CDC2) (BY
FT SIMILARITY).
FT FT 753 753
FT FT PHOSPHORYLATION (BY CDC2) (BY
FT SIMILARITY).
FT FT 759 759
FT FT PHOSPHORYLATION (BY CDC2) (BY
FT SIMILARITY).
FT FT 789 789
FT FT PHOSPHORYLATION (BY CDC2) (BY
FT SIMILARITY).
FT FT 1 24
FT FT MDPERRRELRLKREEMLEAER -> MLGGSGHGRRSL
FT FT AALSQ (IN ISOFORM HELA L-CAD I AND
FT FT ISOFORM HELA L-CAD II).
FT FT MISSING (IN ISOFORM HELA L-CAD I AND
FT FT ISOFORM WI-38 L-CAD I).
FT FT MISSING (IN ISOFORM HELA L-CAD II AND
FT FT ISOFORM WI-38 L-CAD II/1-CAD).
FT FT V -> M (IN REF. 1).
FT FT 793 AA; 93250 MW; 2A0DC63D16DD6B5F CRC64;
SQ SEQUENCE

Query Match 5.1%; Score 7; DB 1; Length 793;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 VSSKRL 77
DB 772 VSSKRL 778
RESULT 24
OXYB_HUMAN
ID OXYB_HUMAN STANDARD; PRT; 807 AA.
AC P22059;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OXYSTEROL-BINDING PROTEIN.
GN OSBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90243258; PubMed-1970801;
RA Levanon D., Hsieh C.L., Franke U., Dawson P.A., Ridgway N.D.,
RA Brown M.S., Goldstein J.L.;
RT "cDNA cloning of human oxysterol-binding protein and localization of
RL the gene to human chromosome 11 and mouse chromosome 19.";
RL Genomics 7:65-74(1990).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF STEROL METABOLISM.
CC -!- BINDS A RANGE OF OXYSTEROLS.
CC -!- SUBUNIT: HOMODIMER OR HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE OSBP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC -----
DR EMBL; M86917; AAA59973.1; -
DR PIR; A34581; A34581.
DR HSSP; P03316; LKXB.
DR MIM; 167040; -
DR InterPro; IPR000648; -
DR InterPro; IPR001849; -
DR Pfam; PF01237; Oxysterol_BP; 1.
DR Pfam; PF00169; PH; 1.
DR PROSITE; PS01013; OSBP; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
FT DOMAIN 93
FT DOMAIN 88 181
FT DOMAIN 88 181
FT SEQUENCE 807 AA; 89420 MW; 2590AM7BCB54FDFB CRC64;
Query Match 5.1%; Score 7; DB 1; Length 807;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 AAFTVSS 73
DB 477 AAFTVSS 483
RESULT 25
OXYB_RABIT
ID OXYB_RABIT STANDARD; PRT; 809 AA.
AC P16258;

```
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OXYSTEROL-BINDING PROTEIN.
GN OSBP.
OS Oryctolagus cuniculus (rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=89380310; PubMed=2777807;
RA Dawson P.A., Ridgway N.D., Slaughter C.A., Brown M.S.,
RA Goldstein J.L.;
RT "cDNA cloning and expression of oxysterol-binding protein, an
RT oligomer with a potential leucine zipper.";
RL J. Biol. Chem. 264:16798-16803(1989).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF STEROL METABOLISM.
CC -!- BINDS A RANGE OF OXYSTEROLS.
CC -!- SUBUNIT: HOMODIMER OR HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE OSBP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC -----
DR EMBL; J05056; AAA31427.1; -
DR PIR; A34404; A34404.
DR InterPro; IPR000648; -
DR InterPro; IPR001849; -
DR Pfam; PF01237; Oxysterol_BP; 1.
DR Pfam; PF00169; PH; 1.
DR PROSITE; PS01013; OSBP; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
FT MOD_RES 1 1 BLOCKED.
FT DOMAIN 1 92 GLY/ALA-RICH.
FT DOMAIN 90 183 PH.
SQ SEQUENCE 809 AA; 89478 MW; 55C6CAE1B985B1E0 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 809;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AAFVSS 73
DB 479 AAFVSS 485
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RESULT 26
FTSK_ECOLI STANDARD; PRT; 1329 AA.
AC F46889; P77450;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELL DIVISION PROTEIN FTSK.
GN FTSK.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=96042098; PubMed=7592387;
```

```
RA Begg K.J., Dewar S.J., Donachie W.D.;
RT "A new Escherichia coli cell division gene, ftsK.";
RL J. Bacteriol. 177:6211-6222(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -!- FUNCTION: REQUIRED FOR SEPTUM FORMATION. MAY BE INVOLVED IN
CC PEPTIDOGLYCAN SYNTHESIS OR MODIFICATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE FTSK/SPOIIIE FAMILY.
CC -----
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CC -----
DR EMBL; Z49932; CAA90178.1; -
DR EMBL; AF000191; AAC73976.1; -
DR EMBL; D90726; BAA35615.1; -
DR EMBL; D90727; BAA35622.1; -
DR EcoGene; EG13226; ftsK.
DR InterPro; IPR002543; -
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
KW Cell division; ATP-binding; Transmembrane.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 112 132 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
FT TRANSMEM 560 580 POTENTIAL.
FT NP_BIND 991 998 ATP (POTENTIAL).
FT MUTAGEN 80 80 G->A: IN TOE44, LOSS OF FUNCTION UNDER
FT EXTREME CONDITIONS.
FT CONFLICT 333 334 WA -> CV (IN REF. 1).
FT CONFLICT 388 389 QP -> HA (IN REF. 1).
FT CONFLICT 1101 1103 DSM -> GQY (IN REF. 1).
FT CONFLICT 1193 1193 A -> R (IN REF. 1).
SQ SEQUENCE 1329 AA; 146662 MW; ED24BF8464481CFC CRC64;

Query Match 5.1%; Score 7; DB 1; Length 1329;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 AFTVSSK 74
DB 1177 AFTVSSK 1183
|||||

RESULT 27
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```
FAS2_SCHPO
ID FAS2_SCHPO STANDARD; PRT: 1842 AA.
AC Q10289; P78973; O14163;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT FATTY ACID SYNTHASE, SUBUNIT ALPHA (EC 2.3.1.86) (P190/210) [INCLUDES:
DE EC 1.1.1.100; EC 2.3.1.41].
GN FAS2 OR LSD1 OR SPAC4A8.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96354912; PubMed=8769419;
RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,
RA Hirata A., Yanagida M.;
RT "Aberrant mitosis in fission yeast mutants defective in fatty acid
RT synthetase and acetyl CoA carboxylase.";
RL J. Cell Biol. 134:949-961(1996).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=972;
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RA Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 1-215 FROM N.A.
RA Koken M.H.M., de Rooij J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 1-20.
RX MEDLINE=94245730; PubMed=8188691;
RA Kaeslin E., Heyer W.-D.;
RT "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand
RT exchange in vitro.";
RL J. Biol. Chem. 269:14103-14110(1994).
CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,
CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-
CC CARRIER-PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING
CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+)
CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + MALONYL-[ACYL-
CC CARRIER PROTEIN] = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + CO(2) +
CC [ACYL-CARRIER PROTEIN].
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
CC NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
CC -1- SUBUNIT: FATTY ACID SYNTHETASE ARE [ALPHA(6)BETA(6)] HEXAMERS OF
CC TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).
CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
CC OTHER FUNGI.
CC -----
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CC -----
DR EMBL; D83412; BAAL1913.1; -.
DR EMBL; Z98762; CAB11481.1; -.
DR EMBL; U82216; AAB39943.1; -.
DR InterPro; IPR000255; -.
DR InterPro; IPR000794; -.
DR InterPro; IPR002582; -.
DR Pfam; PF01648; ACPS; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.

KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
KW Transferrase; NADP; Phosphopantetheine.
FT DOMAIN 1 ? ACYL CARRIER.
FT DOMAIN ? ? BETA-KETOACYL REDUCTASE.
FT DOMAIN ? 1842 BETA-KETOACYL SYNTHASE.
FT BINDING 180 180 PHOSPHOPANTETHEINE (BY SIMILARITY).
FT ACT_SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT CONFLICT 107 107 S -> A (IN REF. 3).
FT CONFLICT 422 422 R -> K (IN REF. 2).
SQ SEQUENCE 1842 AA; 202196 MW; 9FFB63E4FA285FID CRC64;

Query Match 5.1%; Score 7; DB 1; Length 1842;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 SPTAEGG 29
DB 304 SPTAEGG 310

RESULT 28
YPHE_BACSU STANDARD; PRT: 67 AA.
ID YPHE_BACSU
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 7.5 KDA PROTEIN IN GPSA-SPOIVA INTERGENIC REGION.
GN YPHE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the sera and kdg loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -----
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CC -----
DR EMBL; L47648; AAC83968.1; -.
DR EMBL; Z99115; CAB14198.1; -.
DR Subtilist; BG11444; yphE.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 41 61 POTENTIAL.
SQ SEQUENCE 67 AA; 7522 MW; 0A4E3CB4B4E07D14 CRC64;

Query Match 4.3%; Score 6; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 MFLAVA 15
DB 18 MFLAVA 23

RESULT 29
Y055_NPVAC
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ID Y055.NPVAC STANDARD; PRT; 73 AA.
AC P41459;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 8.2 KDA PROTEIN IN LEP8-FP INTERGENIC REGION.
OS Autographa californica nuclear polyhedrosis virus (ACMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RL polyhedrosis virus."
RL Virology 202:586-605(1994).
CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
CC -----
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CC -----
DR EMBL; L22858; AAA66685.1; -.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8190 MW; 0667F3D51E6386E8 CRC64;

Query Match 4.3%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 YKTFEA 67
   |||||
Db 41 YKTFEA 46

RESULT 30
VG10.HSVEB
ID VG10.HSVEB STANDARD; PRT; 100 AA.
AC P28980;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE HYPOTHETICAL GENE 10 PROTEIN.
GN 10.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31520;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1."
RL Virology 189:304-316(1992).
CC -----
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CC -----
DR EMBL; M86664; AAB02445.1; -.
DR PIR; B36796;
KW Hypothetical protein.
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SQ SEQUENCE 100 AA; 10802 MW; B53A8AC6F24BB4C7 CRC64;

Query Match 4.3%; Score 6; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VVLGLA 21
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Db 17 VVLGLA 22
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Search completed: November 19, 2001, 13:12:48
Job time: 183 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 19, 2001, 13:08:54 ; Search time 12.51 Seconds
(without alignments)
248.238 Million cell updates/sec

Title: CAA76556
Perfect score: 138
Sequence: 1 MAHKFWAMFLAVAVLGL.....SEALHIATGPEVHAVKPGA 138

Scoring table:
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Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	8.7	339	1 US-08-433-854-4	Sequence 4, Appli
2	12	8.7	339	1 US-08-174-745A-4	Sequence 4, Appli
3	12	8.7	339	2 US-08-195-947-4	Sequence 4, Appli
4	12	8.7	339	2 US-08-433-885-4	Sequence 4, Appli
5	12	8.7	339	2 US-08-433-908B-4	Sequence 4, Appli
6	12	8.7	339	4 US-08-410-614-4	Sequence 4, Appli
7	11	8.0	21	1 US-08-433-854-11	Sequence 11, Appli
8	11	8.0	21	1 US-08-174-745A-11	Sequence 11, Appli
9	11	8.0	21	2 US-08-195-947-11	Sequence 11, Appli
10	11	8.0	21	2 US-08-433-885-11	Sequence 11, Appli
11	11	8.0	21	2 US-08-433-908B-11	Sequence 11, Appli
12	11	8.0	21	4 US-08-410-614-11	Sequence 11, Appli
13	7	5.1	13	1 US-08-433-854-28	Sequence 28, Appli
14	7	5.1	13	1 US-08-174-745A-28	Sequence 28, Appli
15	7	5.1	13	2 US-08-195-947-28	Sequence 28, Appli
16	7	5.1	13	2 US-08-433-885-28	Sequence 28, Appli
17	7	5.1	13	2 US-08-433-908B-28	Sequence 28, Appli
18	7	5.1	13	4 US-08-410-614-28	Sequence 28, Appli
19	7	5.1	20	1 US-08-440-861-15	Sequence 15, Appli
20	7	5.1	116	1 US-08-285-440-1	Sequence 1, Appli
21	7	5.1	116	1 US-08-630-349-1	Sequence 1, Appli
22	7	5.1	118	1 US-08-285-440-2	Sequence 2, Appli
23	7	5.1	118	1 US-08-630-349-2	Sequence 2, Appli
24	7	5.1	122	1 US-08-285-440-3	Sequence 3, Appli
25	7	5.1	122	1 US-08-630-349-3	Sequence 3, Appli
26	7	5.1	301	1 US-08-440-861-2	Sequence 2, Appli
27	7	5.1	301	1 US-08-433-854-2	Sequence 2, Appli

28	7	5.1	301	1	US-08-174-745A-2	Sequence 2, Appli
29	7	5.1	301	2	US-08-195-947-2	Sequence 2, Appli
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32	7	5.1	301	4	US-08-410-614-2	Sequence 2, Appli
33	7	5.1	308	4	US-08-413-974-2	Sequence 2, Appli
34	7	5.1	308	4	US-08-434-418-2	Sequence 2, Appli
35	7	5.1	308	4	US-08-433-288-2	Sequence 2, Appli
36	7	5.1	308	4	US-08-174-739A-2	Sequence 2, Appli
37	7	5.1	312	1	US-08-285-440-4	Sequence 4, Appli
38	7	5.1	312	1	US-08-630-349-4	Sequence 4, Appli
39	7	5.1	532	1	US-08-285-440-5	Sequence 5, Appli
40	7	5.1	532	1	US-08-630-349-5	Sequence 5, Appli
41	7	5.1	558	1	US-08-285-440-6	Sequence 5, Appli
42	7	5.1	558	1	US-08-630-349-6	Sequence 6, Appli
43	7	5.1	700	2	US-08-568-459A-10	Sequence 10, Appli
44	7	5.1	700	2	US-08-487-826B-10	Sequence 10, Appli
45	7	5.1	2182	2	US-08-487-826B-16	Sequence 16, Appli
46	7	5.1	2627	2	US-08-751-189-3	Sequence 3, Appli
47	7	5.1	2627	2	US-09-060-836-3	Sequence 3, Appli
48	7	5.1	2627	4	US-09-184-445-3	Sequence 14, Appli
49	6	4.3	12	3	US-08-814-836-14	Sequence 23, Appli
50	6	4.3	16	1	US-08-616-133-23	

ALIGNMENTS

RESULT 1
US-08-433-854-4
; Sequence 4, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avlioglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryyn
; APPLICANT: Suphloglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-854-4

Query Match 8.7%; Score 12; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLE 40
| | | | | | | | | |
Db 62 GKATTEQKLE 73

RESULT 2

US-08-174-745A-4
; Sequence 4, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; FILING DATE: 14-AUG-1992

PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992

ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-174-745A-4

Query Match 8.7%; Score 12; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLE 40
| | | | | | | | | |
Db 62 GKATTEQKLE 73

RESULT 3

US-08-195-947-4
; Sequence 4, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:

; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; FILING DATE: 14-AUG-1992

PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992

ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-195-947-4

Query Match 8.7%; Score 12; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLE 40
| | | | | | | | | |
Db 62 GKATTEQKLE 73

RESULT 4

US-08-433-885-4
; Sequence 4, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:

; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,885
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-885-4

Query Match 8.7%; Score 12; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEEQKLE 40
|||||
DB 62 GKATTEEQKLE 73

RESULT 5
US-08-433-908B-4
Sequence 4, Application US/08433908B
Patent No. 5965455
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjologlu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terry
APPLICANT: Suphioglu, Cenik
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,908B
FILING DATE: 02-MAY-1995
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-908B-4

Query Match 8.7%; Score 12; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEEQKLE 40
|||||
DB 62 GKATTEEQKLE 73

RESULT 6
US-08-410-614-4
Sequence 4, Application US/08410614
Patent No. 6277383
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjologlu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terry
APPLICANT: Suphioglu, Cenik
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,947
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-410-614-4

Query Match 8.7%; Score 12; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLE 40
|||||
Db 62 GKATTEQKLE 73

RESULT 7

US-08-433-854-11
; Sequence 11, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-11

Query Match 8.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKATTEQKLE 38
|||||
Db 11 GGRATTEQKL 21

RESULT 8

US-08-174-745A-11
; Sequence 11, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-174-745A-11

Query Match 8.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKATTEQKL 38
|||||
Db 11 GGRATTEQKL 21

RESULT 9

US-08-195-947-11
; Sequence 11, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Lisa D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-195-947-11

Query Match      8.0%; Score 11; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKGATTEQKL 38
Db 11 GKGATTEQKL 21

RESULT 10
US-08-433-885-11
; Sequence 11, Application US/08433885
; Patent No. 5863333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-885-11

Query Match      8.0%; Score 11; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKGATTEQKL 38
Db 11 GKGATTEQKL 21

RESULT 11
US-08-433-908B-11
; Sequence 11, Application US/08433908B
; Patent No. 5965455
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,908B
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-908B-11
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Lisa D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-195-947-11

Query Match      8.0%; Score 11; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKGATTEQKL 38
Db 11 GKGATTEQKL 21

RESULT 10
US-08-433-885-11
; Sequence 11, Application US/08433885
; Patent No. 5863333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
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Query Match 8.0%; Score 11; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKGATTEEQKL 38
|||||
Db 11 GKGATTEEQKL 21

RESULT 12

US-08-410-614-11

; Sequence 11, Application US/08410614

; Patent No. 6277383

; GENERAL INFORMATION:

; APPLICANT: Singh, Mohan Bir

; APPLICANT: Knox, Robert B.

; APPLICANT: Smith, Penelope

; APPLICANT: Avjoglu, Asil

; APPLICANT: Theerakulpisut, Piyada

; APPLICANT: Hough, Terryn

; APPLICANT: Suphioglu, Cenk

; APPLICANT: Ong, Eng Kok

; TITLE OF INVENTION: Ryegrass Pollen Allergen

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/410,614

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/195,947

; FILING DATE: 14-FEB-1994

; APPLICATION NUMBER: US 07/930,060

; FILING DATE: 14-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschutz, Liza D.

; REGISTRATION NUMBER: 33,712

; REFERENCE/DOCKET NUMBER: IMPH-0024

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-410-614-11

Query Match 8.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GKGATTEEQKL 38
|||||
Db 11 GKGATTEEQKL 21

RESULT 13

US-08-433-854-28

; Sequence 28, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,854

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/930,060

; FILING DATE: 14-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschutz, Liza D.

; REGISTRATION NUMBER: 33,712

; REFERENCE/DOCKET NUMBER: IMPH-0024

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-433-854-28

Query Match 5.1%; Score 7; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||
Db 6 EVHAVKP 12

RESULT 14

US-08-174-745A-28

; Sequence 28, Application US/08174745A

; Patent No. 5736362

; GENERAL INFORMATION:

; APPLICANT: Singh, Mohan Bir

; APPLICANT: Knox, Robert B.

; APPLICANT: Smith, Penelope

; APPLICANT: Avjoglu, Asil

; APPLICANT: Theerakulpisut, Piyada

; APPLICANT: Hough, Terryn

; APPLICANT: Suphioglu, Cenk

; APPLICANT: Ong, Eng Kok

; TITLE OF INVENTION: Ryegrass Pollen Allergen

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-174-745A-28

Query Match 5.1%; Score 7; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
Db 6 EVHAVKP 12
|||||

RESULT 15
US-08-195-947-28
; Sequence 28, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-174-745A-28

Query Match 5.1%; Score 7; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
Db 6 EVHAVKP 12
|||||

RESULT 16
US-08-433-885-28
; Sequence 28, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-195-947-28
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US-08-433-885-28

Query Match 5.1%; Score 7; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||||
Db 6 EVHAVKP 12

RESULT 17

US-08-433-908B-28
; Sequence 28, Application US/08433908B
; Patent No. 5965455
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,908B
FILING DATE: 02-MAY-1995

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D4
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-908B-28

Query Match 5.1%; Score 7; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||||
Db 6 EVHAVKP 12

RESULT 18

US-08-410-614-28
; Sequence 28, Application US/08410614
; Patent No. 6277383
; GENERAL INFORMATION:

; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,947
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-410-614-28

Query Match 5.1%; Score 7; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||||
Db 6 EVHAVKP 12

RESULT 19

US-08-440-861-15
; Sequence 15, Application US/08440861
; Patent No. 5710126
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Lugman, Mohammad
; TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

```
;
;
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,861
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,016
; FILING DATE: 31-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-440-861-15
;
;
; Query Match 5.1%; Score 7; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 2;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 130 EVHAVKP 136
; DB 6 EVHAVKP 12
;
;
; RESULT 20
; US-08-285-440-1
; Sequence 1, Application US/08285440
; Patent No. 5532337
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,440
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/859,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
```

```
;
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-285-440-1
;
; Query Match 5.1%; Score 7; DB 1; Length 116;
; Best Local Similarity 100.0%; Pred. No. 10;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 71 VSSKRNL 77
; DB 95 VSSKRNL 101
;
; RESULT 21
; US-08-630-349-1
; Sequence 1, Application US/08630349
; Patent No. 5739008
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,349
; FILING DATE: April 10, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,440
; FILING DATE: August 4, 1994
; APPLICATION NUMBER: 07/858,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-349-1

Query Match 5.1%; Score 7; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 VSSKRNL 77
Db 95 VSSKRNL 101

RESULT 22
US-08-285-440-2
; Sequence 2, Application US/08285440
; Patent No. 5532337
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,440
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/858,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-2

Query Match 5.1%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 VSSKRNL 77
Db 97 VSSKRNL 103

RESULT 23
US-08-630-349-2
; Sequence 2, Application US/08630349
; Patent No. 5739008
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS

;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/630,349
;; FILING DATE: April 10, 1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/285,440
;; FILING DATE: August 4, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/858,947
;; FILING DATE: March 27, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-630-349-2

Query Match 5.1%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 VSSKRNL 77
|||||||
Db 97 VSSKRNL 103

RESULT 24
US-08-285-440-3
; Sequence 3, Application US/08285440
; Patent No. 5532337
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,440
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/858,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-3

Query Match 5.1%; Score 7; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 VSSKRNL 77
|||||||
Db 101 VSSKRNL 107

RESULT 25
US-08-630-349-3
; Sequence 3, Application US/08630349
; Patent No. 5739008
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,349

; FILING DATE: April 10, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,440
; FILING DATE: August 4, 1994
; PRIOR APPLICATION DATA: 07/858,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-630-349-3

Query Match 5.1%; Score 7; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 VSSKRN 77
Db 101 VSSKRN 107

RESULT 26
US-08-440-861-2
; Sequence 2, Application US/08440861
; Patent No. 5710126
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Luqman, Mohammad
; TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
; TITLE OF INVENTION: ALLERGEN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,861
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,016
; FILING DATE: 31-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-440-861-2

Query Match 5.1%; Score 7; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
Db 151 EVHAVKP 157

RESULT 27
US-08-433-854-2
; Sequence 2, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-433-854-2

Query Match 5.1%; Score 7; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
Db 151 EVHAVKP 157

RESULT 28
US-08-174-745A-2

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-885-2

Query Match 5.1%; Score 7; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
|||||
Db 151 EVHAVKP 157

Search completed: November 19, 2001, 13:09:43
Job time: 49 sec

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; Sequence 2, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-174-745A-2

Query Match          5.1%; Score 7; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
   |||||
Db 151 EVHAVKP 157

RESULT 29
US-08-195-947-2
; Sequence 2, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-947-2

Query Match          5.1%; Score 7; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
   |||||
Db 151 EVHAVKP 157

RESULT 30
US-08-433-885-2
; Sequence 2, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
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STIC-ILL

On 8.8.16

From: Huynh, Phuong N.
Sent: Monday, November 19, 2001 12:30 PM
To: STIC-ILL
Subject: RE: 09/696,169

Please deliver the following:

Int Arch Allergy Immunol 1995 Sep;108(1):49-54

J Allergy Clin Immunol 1996 Mar;97(3):781-7

Thanks,

Neon
Art unit 1644
Mail CM1, 9E12
Office CM1, 9D06
Tel 308-4844

```
!!AA_SEQUENCE 1.0
CAA76556 GB:Y16955 p1 p6 allergen [Phleum pratense] (ver 1)
CAA76556 Length: 138 November 19, 2001 13:06 Type: P Check: 8085 ..
      1 MAAHKFWAM FLAVAVVLGL ATSPTEGGK ATTEOKLIE DINASFRAAM
     51 ATTANVPPAD KYKTEAAFT VSKRNLADA VSKAPOLVPK LDEVYNAAYN
    101 AADHAAPEDK YEAFVLHFE ALHIIAGTPE VHAVKPGA
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; TOIG of: caa76556 check: 8085 from: 1 to: 138
; CAA76556 GB:Y16955 Phl p6 allergen [Phleum pratense] (ver 1)
; CAA76556 Length: 138 November 19, 2001 13:06 Type: P Check: 8085
caa76556
MAAHKFMVAMFLAVAVVLGLATSPTEGGKATTEBQKLIEDINASFRAAMATTANVPADKYKTFEAAFT
VSSKRNLDADVSKAPQLVPKLDDEVINAAINADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVKPGAI
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 13:09:00 ; Search time 14.36 Seconds
(without alignments)
732.040 Million cell updates/sec

Title: CAA76556
Perfect score: 138
Sequence: 1 MAHKFWAMFLAVVVLG.....SEALHIAGTPEVHAVKPGA 138

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	58.0	132	2	pollen allergen ph
2	17	12.3	264	2	allergen V - velve
3	15	10.9	280	2	allergen Phl p Vb
4	12	8.7	257	2	PHLP5A protein - c
5	12	8.7	312	2	allergen Phl p v p
6	12	8.7	339	1	group-V allergen i
7	11	8.0	28	2	pollen allergen DG
8	9	6.5	116	2	NADH dehydrogenase
9	8	5.8	221	2	hypothetical prote
10	8	5.8	255	2	probable short-cha
11	8	5.8	443	2	omega-3 fatty acid
12	8	5.8	503	2	probable sodium-tr
13	8	5.8	578	2	transmembrane prot
14	8	5.8	765	2	hypothetical prote
15	7	5.1	118	2	ribosomal protein
16	7	5.1	183	2	ribulose-bisphosph
17	7	5.1	189	2	hypothetical prote
18	7	5.1	195	1	morphogenetic prot
19	7	5.1	308	2	pollen allergen PI
20	7	5.1	315	2	probable CCH-type
21	7	5.1	333	2	allergen Poa p IX
22	7	5.1	348	2	probable oxidoredu
23	7	5.1	351	2	conserved hypothet
24	7	5.1	378	2	manganese peroxida
25	7	5.1	380	2	probable isomerase
26	7	5.1	406	2	probable cation ex
27	7	5.1	418	2	pantothenate metab
28	7	5.1	421	2	CLP proteinase ATP
29	7	5.1	421	2	ATP-dependent Clp

ALIGNMENTS

```
RESULT 1
S38585 pollen allergen Phl p VI precursor - common timothy
C:Species: Phleum pratense (common timothy)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S38585
R:Petersen, A.; Bufer, A.; Schramm, G.; Schlaak, M.; Becker, W.
submitted to the EMBL Data Library, November 1993
A:Description: Phl p VI - a major allergen of timothy grass (Phleum pratense) pollen
A:Reference number: S38585
A:Accession: S38585
A:Molecule type: mRNA
A:Residues: 1-132 <PET>
A:Cross-references: EMBL:Z27082; NID:q414711; PIDN:CAA81608.1; PID:q414712
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-132/Product: pollen allergen Phl p VI #status predicted <MAT>

Query Match 58.0%; Score 80; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.8e-72;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 NASFRAMATTANVPADKYKTFEAAFTVSSKRNLAADVSKAPOLVPKLDVYNAAYNAA 102
Db 37 NASFRAMATTANVPADKYKTFEAAFTVSSKRNLAADVSKAPOLVPKLDVYNAAYNAA 96
|||||
QY 103 DHAAPEDKYEAFVLFHFEAL 122
Db 97 DHAAPEDKYEAFVLFHFEAL 116
|||||

RESULT 2
T09449 allergen V - velvet grass (fragment)
C:Species: Holcus lanatus (velvet grass)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T09449
R:Schramm, G.; Bufer, A.; Petersen, A.; Schlaak, M.; Becker, W.
Eur. J. Biochem. 252, 200-206, 1998
A:Title: Molecular and immunological characterization of group V allergen isoforms fr
A:Reference number: Z16674; MUID:98181862
A:Accession: T09449
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-264 <SCH>
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A:Cross-references: EMBL:Z97874; NID:g2266624; PIDN:CAB10765.1; PID:g2266625
C:Superfamily: grass pollen allergen IX

Query Match 12.3%; Score 17; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ANVPPADKYKTFEAAFT 70
|||||
DB 42 ANVPPADKYKTFEAAFT 58

RESULT 3
S38584

allergen Phl p Vb - common timothy
A:Species: Phleum pratense (common timothy)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C:Accession: S38584
R:Bufo, A.; Becker, W.; Petersen, A.; Schramm, G.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Major allergen Phl p Vb is highly homologous to a pathogenesis related protein
A:Reference number: S38584
A:Accession: S38584
A:Status: preliminary
A:Superfamily: grass pollen allergen IX
A:Molecule type: mRNA
A:Residues: 1-280 <BUF>
A:Cross-references: EMBL:Z27083; NID:g414709; PID:g414710
C:Superfamily: grass pollen allergen IX
C:Keywords: pollen

Query Match 10.3%; Score 15; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIEDIN 43
|||||
DB 35 GKATTEQKLIEDIN 49

RESULT 4
S32101

PHLP5A protein - common timothy (fragment)
A:Species: Phleum pratense (common timothy)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995
C:Accession: S32101
R:Bufo, A.; Becker, W.M.; Petersen, A.; Schramm, G.; Schlaak, M.
submitted to the EMBL Data Library, February 1993
A:Description: Phl pV (timothy grass) major allergen bears at least two B-cell epitopes.
A:Reference number: S32101
A:Accession: S32101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-257 <BUF>
A:Cross-references: EMBL:X70942
C:Superfamily: grass pollen allergen IX

Query Match 8.7%; Score 12; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIIE 40
|||||
DB 5 GKATTEQKLIIE 16

RESULT 5
S37400

allergen Phl p V precursor - common timothy
N:Alternate names: 38K allergen; Phlp5 protein
C:Species: Phleum pratense (common timothy)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S37400; S38293

R:Vitale, S.

submitted to the EMBL Data Library, August 1993

A:Reference number: S37400

A:Accession: S37400

A:Molecule type: mRNA

A:Residues: 1-312 <VRT>

A:Cross-references: EMBL:X74735; NID:g398829; PIDN:CAA52753.1; PID:g398830

R:Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.

Biol. Chem. Hoppe-Seyler 374, 855-861, 1993

A:Title: Comparison of four grass pollen species concerning their allergens of grass

A:Reference number: S38288; MUID:94092339

A:Accession: S38293

A:Molecule type: protein

A:Residues: 26-45 <PET>

C:Superfamily: grass pollen allergen IX

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-312/Product: allergen Phl p V #status predicted <MAT>

Query Match 8.7%; Score 12; DB 2; Length 312;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIIE 40
|||||
DB 57 GKATTEQKLIIE 68

RESULT 6
JT0756

group-V allergen isoform, Lol p VB precursor (clone 19R) - perennial ryegrass
N:Alternate names: 34K allergen

C:Species: Lolium perenne (perennial ryegrass)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JT0756; S38289

R:Ong, E.K.; Griffith, I.J.; Knox, R.B.; Singh, M.B.

Gene 134, 235-240, 1993

A:Title: Cloning of a cDNA encoding a group-V (group-IX) allergen isoform from rye-gr

A:Reference number: JT0756; MUID:94085783

A:Accession: JT0756

A:Molecule type: mRNA

A:Residues: 1-339 <ONG>

A:Cross-references: GB:L13083; NID:g455287; PIDN:AAA33405.1; PID:g455288

R:Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.

Biol. Chem. Hoppe-Seyler 374, 855-861, 1993

A:Title: Comparison of four grass pollen species concerning their allergens of grass

A:Reference number: S38288; MUID:94092339

A:Accession: S38289

A:Molecule type: protein

A:Residues: 26-44 <PET>

C:Superfamily: grass pollen allergen IX

C:Keywords: pollen

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-339/Product: group-V allergen isoform, Lol p VB #status experimental <MAT>

Query Match 8.7%; Score 12; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIIE 40
|||||
DB 62 GKATTEQKLIIE 73

RESULT 7
A60359

pollen allergen DG3 - orchard grass (fragment)

C:Species: Dactylis glomerata (orchard grass)

C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Nov-2000

C:Accession: A60359

R;Walsh, D.J.; Matthews, J.A.; Denmeade, R.; Maxwell, P.; Davidson, M.; Walker, M.R.
Int. Arch. Allergy Appl. Immunol. 91, 419-425, 1990
A:Title: Monoclonal antibodies to proteins from cocksfoot grass (Dactylis glomerata) pol
A:Reference number: A60359; MUID:91007970
A:Accession: A60359
A:Molecule type: protein
A:Residues: 1-28 <WAL>
C:Superfamily: grass pollen allergen IX
C:Keywords: pollen

Query Match 8.0%; Score 11; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGGATTEEQKL 38
|||||
DB 11 GGGATTEEQKL 21

RESULT 8
S01507
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - sea urchin (Strongylocentrotus pu
C:Species: mitochondrion Strongylocentrotus purpuratus (purple urchin)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 07-Dec-1999
C:Accession: S01507
R;Jacobs, H.T.; Elliott, D.J.; Math, V.B.; Farquharson, A.
J. Mol. Biol. 202, 185-217, 1998
A:Title: Nucleotide sequence and gene organization of sea urchin mitochondrial DNA.
A:Reference number: S01499; MUID:9011951
A:Accession: S01507
A:Molecule type: DNA
A:Residues: 1-116 <JAC>
A:Cross-references: EMBL:X12631; NID:g296545; PIDN:CAA311158.1; PID:g13673
C:Genetics:
A:Gene: nd3
A:Genome: mitochondrion
A:Genetic code: SGC8
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.5%; Score 9; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVAVVLGLA 21
|||||
DB 13 AVAVVLGLA 21

RESULT 9
C64040
hypothetical protein HI1681 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: C64040
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: C64040
A:Molecule type: DNA
A:Residues: 1-221 <TIGR>
A:Cross-references: GB:U32841; GB:I42023; NID:gl574529; PIDN:AAC23327.1; PID:gl574533; T

Query Match 5.8%; Score 8; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AVVLGLAT 22
|||||
DB 5 AVVLGLAT 12

RESULT 10
D83416
probable short-chain dehydrogenase PA1828 [imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83416
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: AB2950; MUID:20437337
A:Accession: D83416
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <STO>
A:Cross-references: GB:AE004609; GB:AE004091; NID:g9947810; PIDN:AAG05217.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1828
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 5.8%; Score 8; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 TAEGGKAT 32
|||||
DB 56 TAEGGKAT 63

RESULT 11
T01697
omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
C:Species: Zea mays (maize)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01697
R;Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T.
Plant Mol. Biol. 36, 297-306, 1998
A:Title: Two maize genes encoding omega-3 fatty acid desaturase and their differentia
A:Reference number: Z14400; MUID:98145435
A:Accession: T01697
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-443 <BER>
A:Cross-references: EMBL:D63954; NID:g2446997; PIDN:BAA22441.1; PID:g2446998
A:Experimental source: strain honey bantum
C:Genetics:
A:Gene: FAD7
A:Introns: 163/2; 193/2; 215/3; 246/3; 308/3; 335/3; 381/3
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 5.8%; Score 8; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VAVVLGLA 21
|||||
DB 123 VAVVLGLA 130

RESULT 12
B81690

probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) nqrB chain TD
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
C:Accession: B81690
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberq, J.F.; White, O.; Hickey,
C.; Dodson, R.; Winn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255
A:Accession: B81690
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-503 <TET>
A:Cross-references: GB:AE002323; GB:AE002160; NID:g7190585; PIDN:AAF39389.1; PID:g7190589
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0550
C:Keywords: oxidoreductase

Query Match 5.8%; Score 8; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TSPTAEGG 29
|||||||
DB 313 TSPTAEGG 320

RESULT 13
T03475
transmembrane protein - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Aug-1999
R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus S81003
A:Reference number: Z14955; MUID:97404404
A:Accession: T03475
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-578 <VIC>
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16128.1; PID:g3128276
C:Genetics:
A:Map position: 1
C:Superfamily: proline carrier protein
C:Keywords: transmembrane protein

Query Match 5.8%; Score 8; DB 2; Length 578;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VAVVLGLA 21
|||||||
DB 442 VAVVLGLA 449

RESULT 14
G64502
hypothetical protein MJ1626 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: G64502
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: G64502

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-765 <BUL>
A:Cross-references: GB:U67602; GB:L77117; NID:gi592214; PIDN:AAB99649.1; PID:gi500524
C:Genetics:
A:Map position: REV1602382-1600085

Query Match 5.8%; Score 8; DB 2; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTEQKLI 39
|||||||
DB 750 TTEQKLI 757

RESULT 15
E69696
ribosomal protein L19 rplS - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E69696
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Teropstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033
A:Accession: E69696
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-118 <RUN>
A:Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13477.1; PID:g26339
A:Experimental source: strain 168
C:Genetics:
A:Gene: rplS
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 5.1%; Score 7; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QKLIEDI 42
|||||||
DB 5 QKLIEDI 11

RESULT 16
S54818
ribulose-bisphosphate carboxylase (EC 4.1.1.39) precursor - prince's feather
C:Species: Amaranthus hybridus var. erythrochachys (prince's feather)
C:Date: 08-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S54818
R:Villegas-Sepulveda, N.; Jofre y Garfias, A.; Jimenez-Moralla, B.; Herrera-Estrella,
submitted to the EMBL Data Library, May 1995
A:Description: Evidence for cis acting elements and trans acting protein factors in t
hypochoondriacus.
A:Reference number: S54818
A:Accession: S54818
A:Molecule type: mRNA
A:Residues: 1-183 <VIL>

A:Cross-references: EMBL:X87171; NID:9809532; PIDN:CAA60636.1; PID:9809533
 A:Note: the source is designated as *Ananthurus hypochoandriacus*
 C:Superfamily: ribulose-bisphosphate carboxylase small chain
 C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 5.1%; Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 AAMATTA 54

DB 9 AAMATTA 15

RESULT 17

D84303
 hypothetical protein Vng1492c [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: D84303
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon, K.H.; Alam, M.; Freitas, T.; Jung, K.H.; Acad. Sci. U.S.A. 97, 12176-12181, 2000.
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483
 A:Accession: D84303
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <STO>
 A:Cross-references: GB:AE004437; NID:g10580988; PIDN:AAG19792.1; GSPDB:GN00138
 A:Gene: VNG1492C

Query Match 5.1%; Score 7; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 RAAMATT 53

DB 82 RAAMATT 88

RESULT 18

YHBP6
 morphogenetic protein - phage phi-6
 N:Alternate names: P12 protein
 C:Species: phage phi-6
 A:Note: host *Pseudomonas phaseolicola*
 C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
 C:Accession: B23368
 R:McGraw, T.; Mindich, L.; Frangione, B.
 J. Virol. 58, 142-151, 1986
 A:Title: Nucleotide sequence of the small double-stranded RNA segment of bacteriophage phi-6.
 A:Reference number: A93017; MUID:86144085
 A:Accession: B23368
 A:Molecule type: genomic RNA
 A:Residues: 1-195 <MCG>
 A:Cross-references: GB:M12921; NID:g215492; PIDN:AAA32359.1; PID:g215494
 C:Genetics:
 A:Gene: P12
 A:Map position: segment S
 C:Superfamily: phage phi-6 morphogenetic protein

Query Match 5.1%; Score 7; DB 1; Length 195;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVAVVIG.19

DB 44 AVAWLIG 50

RESULT 19

A38582
 pollen allergen p1b precursor - perennial ryegrass
 N:Alternate names: 30K allergen
 C:Species: Lolium perenne (perennial ryegrass)
 C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-May-1999
 C:Accession: A38582; S38290
 R:Singh, M.B.; Hough, T.; Theerakulpisut, P.; Avjiloglu, A.; Davies, S.; Smith, P.M.; Proc. Natl. Acad. Sci. U.S.A. 88, 1384-1388, 1991
 A:Title: Isolation of cDNA encoding a newly identified major allergenic protein of ryegrass.
 A:Reference number: A38582; MUID:91142177
 A:Accession: A38582
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-308 <SIN>
 A:Cross-references: GB:M59163
 R:Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
 Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
 A:Title: Comparison of four grass pollen species concerning their allergens of grass pollen.
 A:Reference number: S38288; MUID:94092339
 A:Accession: S38290
 A:Molecule type: protein
 A:Residues: 26-45 <PEW>
 C:Superfamily: grass pollen allergen IX
 C:Keywords: pollen
 F:1-25/domain: signal sequence #status predicted <SIG>
 F:26-308/Product: pollen allergen p1b #status experimental <MAT>

Query Match 5.1%; Score 7; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136

DB 151 EVHAVKP 157

RESULT 20

B84654
 probable CCH-type zinc finger protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: B84654
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: B84654
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-315 <STO>
 A:Cross-references: GB:AE002093; NID:g3643609; PIDN:AAC42256.1; GSPDB:GN00139
 C:Genetics:
 A:Map position: 2

Query Match 5.1%; Score 7; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GLATSPT 25

DB 207 GLATSPT 213

RESULT 21

A39098
allergen Poa p IX (clone 41) - Kentucky bluegrass
C:Species: Poa pratensis (Kentucky bluegrass)
C:Date: 27-Nov-1991 #sequence_revision 03-Apr-1992 #text_change 20-Aug-1999
C:Accession: A39098
R:Silvanovich, A.; Astwood, J.; Zhang, L.; Olsen, E.; Kisil, F.; Sehon, A.; Mohapatra, S.
J. Biol. Chem. 266, 1204-1210, 1991
A:Title: Nucleotide sequence analysis of three cDNAs coding for Poa p IX isoallergens of
A:Reference number: A39098; MUID:91093232
A:Accession: A39098
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-333 <SIL>
A:Cross-references: GB:M38343; NID:g169628; PIDN:AAA63456.1; PID:g169629
A:Note: the authors translated the codon GGG for residue 296 as Ser
C:Superfamily: grass pollen allergen IX
C:Keywords: pollen

Query Match 5.1%; Score 7; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136

|||||

Db 170 EVHAVKP 176

RESULT 22

D75368
probable oxidoreductase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: D75368
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: D75368
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <WHI>
A:Cross-references: GB:AE002009; GB:AE000513; NID:g6459430; PIDN:AAF11227.1; PID:g645943
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI673
A:Map position: 1

Query Match 5.1%; Score 7; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 SPTAEGG 29

|||||

Db 237 SPTAEGG 243

RESULT 23

E69218
conserved hypothetical protein MTH887 - Methanobacterium thermoautotrophicum (strain Del
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
C:Accession: E69218
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514

A:Accession: E69218
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-351 <MTH>
A:Cross-references: GB:AE000864; GB:AE000566; NID:g2621970; PIDN:AAB85385.1; PID:g262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH887
A:Start codon: TTG
C:Superfamily: conserved hypothetical protein MTH887

Query Match 5.1%; Score 7; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FLAVAVV 17

|||||

Db 24 FLAVAVV 30

RESULT 24

A33271
manganese peroxidase (EC 1.11.1.13) Mnp-1 precursor - basidiomycete (Phanerochaete ch
N:Alternate names: lignin peroxidase mnp-1, manganese-dependent
C:Species: Phanerochaete chrysosporium
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 07-Nov-1997
C:Accession: JN0092; A33271
R:Godfrey, B.J.; Mayfield, M.B.; Brown, J.A.; Gold, M.H.
Gene 93, 119-124, 1990
A:Title: Characterization of a gene encoding a manganese peroxidase from Phanerochaete
A:Reference number: JN0092; MUID:91033001
A:Accession: JN0092
A:Molecule type: DNA
A:Residues: 1-378 <GOD>
A:Cross-references: GB:J04980
R:Pribnow, D.; Mayfield, M.B.; Nipper, V.J.; Brown, J.A.; Gold, M.H.
J. Biol. Chem. 264, 5036-5040, 1989
A:Title: Characterization of a cDNA encoding a manganese peroxidase, from the lignin-
A:Reference number: A33271; MUID:89174785
A:Accession: A33271
A:Molecule type: mRNA
A:Residues: 1-378 <PRI>
A:Cross-references: GB:J04624
C:Genetics:
A:Gene: mnp-1
A:Introns: 40/3; 57/1; 80/2; 139/3; 213/3; 352/1
C:Superfamily: lignin peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; manganese; oxidoreductase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:97,152,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.1%; Score 7; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 ASFRAAM 50

|||||

Db 288 ASFRAAM 294

RESULT 25

A71181
probable isomerase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: A71181
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil
A:Reference number: A71000; MUID:98344137

A:Accession: A71181
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-380 <RAW>
 A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30840.1; PID:g3258157
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PHI726
 C:Superfamily: aconitate hydratase

Query Match 5.1%; Score 7; DB 2; Length 380;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VAVVLGL 20
 |||||
 Db 129 VAVVLGL 135

RESULT 26
 H75527
 Probable cation exchanger - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: H75527
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: H75527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-406 <WHI>
 A:Cross-references: GB:AE001897; GB:AE000513; NID:g6458045; PIDN:AAF09952.1; PID:g645805
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0373
 A:Map position: 1
 C:Superfamily: Ca2+/H+-exchanging protein

Query Match 5.1%; Score 7; DB 2; Length 406;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LAVAVVL 18
 |||||
 Db 169 LAVAVVL 175

RESULT 27
 E70899
 Pantothenate metabolism flavoprotein dfp - Mycobacterium tuberculosis (strain H37RV)
 N:Alternate names: probable aspartate 1-decarboxylase activase
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: E70899
 R:Coile, S.T.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 Connor, R.; Bross, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70899
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-418 <COL>
 A:Cross-references: GB:Z80108; GB:AL123456; NID:g3256012; PIDN:CAB02174.1; PID:g1542899

A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: dfp
 C:Superfamily: pantothenate metabolism flavoprotein dfp

Query Match 5.1%; Score 7; DB 2; Length 418;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 LADAVSK 83
 |||||
 Db 263 LADAVSK 269

RESULT 28
 D86596
 CLP proteinase ATPase [imported] - Chlamydophila pneumoniae (strain J138)
 C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: D86596
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349
 A:Accession: D86596
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-421 <STO>
 A:Cross-references: GB:BA000008; NID:g9879220; PIDN:BAA99054.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: clpX
 C:Superfamily: heat shock protein hslu; FtsH/SEC18/CDC48-type ATP-binding domain homo

Query Match 5.1%; Score 7; DB 2; Length 421;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TTANVPP 58
 |||||
 Db 221 TTANVPP 227

RESULT 29
 F72028
 ATP-dependent Clp proteinase, ATP-binding regulatory chain ClpX CP1023 [imported] - C
 C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: F72028; B81512
 R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606
 A:Accession: F72028
 A:Molecule type: DNA
 A:Residues: 1-421 <ARN>
 A:Cross-references: GB:AE001665; GB:AE001363; NID:g4377155; PIDN:ADI8984.1; PID:g437
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
 A:Reference number: A81500; MUID:20150255
 A:Accession: B81512
 A:Molecule type: DNA
 A:Residues: 1-421 <REA>
 A:Cross-references: GB:AE002259; GB:AE002161; NID:g7189932; PIDN:AAF38799.1; PID:g718
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: clpX; CP1023
 C:Superfamily: heat shock protein hslu; FtsH/SEC18/CDC48-type ATP-binding domain homo

Query Match 5.1%; Score 7; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TTANVPP 58
|||||
Db 221 TTANVPP 227

RESULT 30
H86078
PTS system, fructose-like enzyme IIBC component [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: H86078
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H86078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <STO>
A:Cross-references: GB:AE005174; NID:gl2518794; PIDN:AAG59092.1; GSPDB:GN00145; UWGP:254
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: frvB

Query Match 5.1%; Score 7; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AVVLGLA 21
|||||
Db 235 AVVLGLA 241

Search completed: November 19, 2001, 13:10:05
Job time: 65 sec

STIC-ILL

QR180.56

From: Huynh, Phuong N.
Sent: Monday, November 05, 2001 2:46 PM
To: STIC-ILL
Subject: RE: 09/696,169

LPL

Please deliver the following:

Int Arch Allergy Immunol 108: 55-?; 1995

J Immunol 151: 4773-?; 1993

J Immunol 163(10): 5489-96; 1999

J Immunol 162(4): 2406-14;

Thanks,

Neon
Art unit 1644
Mail CM1, 9E12
Office CM1, 9D06
Tel 308-4844

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XX Kay AB, Larche M;
PI WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
XX Example 6; Page 66; 117pp; English.
XX This invention describes a novel method of desensitizing a patient to a
XX polypeptide allergen and comprises administering to the patient a peptide
XX derived from the allergen where restriction to a MHC Class II molecule
XX possessed by the patient can be demonstrated for the peptide and the
XX peptide is able to induce a late phase response in an individual who
XX possesses the MHC Class II molecule. The methods can be used for
XX desensitizing patients to allergens present in e.g. grass, tree and weed
XX (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX produce immunological vaccines which may be used to prevent and/or treat
XX conditions involving hypersensitivity to allergens. This sequence
XX represents a Phleum sp. (Timothy grass) Phl p 6 allergen.
XX Sequence 138 AA;
SQ
Query Match 100.0%; Score 138; DB 20; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.2e-131;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAHKFMVAMFLAVAVVGLATSPATAGGKATTEEQKLIEDINASFRAAMATTANVPAD 60
DB 1 maahkfmvamflavavvlglatspataggkattteeqkliedinasframattanvpad 60
QY 61 KYKTFEAAFTVSSKRNLDADVSKAPQLVPKLDVYNAAYNAADHAAPEDKYEAFVLHSE 120
DB 61 kyktfeaaftvsskrnladvskapqlvpkldevynaaynaadhaapedkyearfvlhse 120
QY 121 ALHIIAGTPEVHAVKPGA 138
DB 121 alhiiagtpevhavkpga 138
RESULT 2
AAY25638
ID AAY25638 standard; protein; 80 AA.
XX AC AAY25638;
XX DT 30-SEP-1999 (first entry)
XX DE Phleum sp. allergen Phl p 6 protein fragment #3.
XX Major histocompatibility complex; class II; desensitising; human;
XX allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
XX chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX Phleum sp.
XX WO9934826-A1.
XX 15-JUL-1999.
XX 11-JAN-1999; 99WO-GB000080.
XX 21-SEP-1998; 98GB-0020474.
XX 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

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XX Kay AB, Larche M;
PI WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
XX Example 6; Page 65-66; 117pp; English.
XX This invention describes a novel method of desensitizing a patient to a
XX polypeptide allergen and comprises administering to the patient a peptide
XX derived from the allergen where restriction to a MHC Class II molecule
XX possessed by the patient can be demonstrated for the peptide and the
XX peptide is able to induce a late phase response in an individual who
XX possesses the MHC Class II molecule. The methods can be used for
XX desensitizing patients to allergens present in e.g. grass, tree and weed
XX (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX produce immunological vaccines which may be used to prevent and/or treat
XX conditions involving hypersensitivity to allergens. This sequence
XX represents a Phleum sp. (Timothy grass) Phl p 6 allergen.
XX Sequence 80 AA;
SQ
Query Match 58.0%; Score 80; DB 20; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.8e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 ADKYKTFEAAFTVSSKRNLDADVSKAPQLVPKLDVYNAAYNAADHAAPEDKYEAFVLH 118
DB 1 adkyktfeaaftvsskrnladvskapqlvpkldevynaaynaadhaapedkyearfvlhf 60
QY 119 SEALHIIAGTPEVHAVKPGA 138
DB 61 sealhiiagtpevhavkpga 80
RESULT 3
AAY25641
ID AAY25641 standard; protein; 132 AA.
XX AC AAY25641;
XX DT 30-SEP-1999 (first entry)
XX DE Phleum sp. allergen Phl p 6 protein fragment #6.
XX Major histocompatibility complex; class II; desensitising; human;
XX allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
XX chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX Phleum sp.
XX WO9934826-A1.
XX 15-JUL-1999.
XX 11-JAN-1999; 99WO-GB000080.
XX 21-SEP-1998; 98GB-0020474.
XX 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 13:08:54 ; Search time 21.15 Seconds
(without alignments)
395.561 Million cell updates/sec

Title: CAA76556
Perfect score: 138
Sequence: 1 MAHKPMVAMFLAVVVLGL.....SEALHIAGTPEVHAVKPGA 138

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
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8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	138	20 AAY25640	Phleum sp. allerg
2	80	58.0	132	20 AAY25638	Phleum sp. allerg
3	80	58.0	132	20 AAY25641	Phleum sp. allerg
4	80	58.0	138	20 AAY25636	Phleum sp. allerg
5	57	41.3	57	20 AAY25637	Phleum sp. allerg
6	57	41.3	106	20 AAY25639	Phleum sp. allerg
7	15	10.9	137	19 AAW76447	Graminae pollen al
8	15	10.9	182	19 AAW76446	Graminae pollen al
9	15	10.9	241	19 AAW76448	Graminae pollen al
10	15	10.9	265	19 AAW76442	Graminae pollen al
11	15	10.9	265	19 AAW76444	Graminae pollen al

12	15	10.9	265	19 AAW76445	Graminae pollen al
13	15	10.9	265	20 AAY25621	Phleum sp. allerg
14	15	10.9	280	20 AAY25628	Phleum sp. allerg
15	15	10.9	280	20 AAY25632	Phleum sp. allerg
16	15	10.9	281	20 AAY25627	Phleum sp. allerg
17	15	10.9	284	20 AAY25625	Phleum sp. allerg
18	15	10.9	284	20 AAY25617	Phleum sp. allerg
19	15	10.9	287	20 AAY25619	Phleum sp. allerg
20	15	10.9	290	20 AAY25620	Phleum sp. allerg
21	15	10.9	295	20 AAY25622	Phleum sp. allerg
22	14	10.1	265	19 AAW76443	Graminae pollen al
23	12	8.7	12	19 AAW76455	Graminae pollen al
24	12	8.7	257	20 AAY25630	Phleum sp. allerg
25	12	8.7	276	20 AAY25615	Phleum sp. allerg
26	12	8.7	276	20 AAY25616	Phleum sp. allerg
27	12	8.7	276	20 AAY25624	Phleum sp. allerg
28	12	8.7	285	20 AAY25633	Phleum sp. allerg
29	12	8.7	286	20 AAY25626	Phleum sp. allerg
30	12	8.7	286	20 AAY25618	Phleum sp. allerg
31	12	8.7	312	20 AAY25629	Phleum sp. allerg
32	12	8.7	312	20 AAY25631	Phleum sp. allerg
33	12	8.7	312	20 AAY25635	Phleum sp. allerg
34	12	8.7	312	20 AAY25623	Sequence of Lol p
35	12	8.7	339	14 AAR33556	Lolium sp. allerg
36	12	8.7	339	20 AAY25602	Lolium sp. allerg
37	12	8.7	339	20 AAY25603	Lolium sp. allerg
38	11	8.0	12	19 AAW76456	Graminae pollen al
39	10	7.2	12	19 AAW76454	Graminae pollen al
40	8	5.8	12	19 AAW76457	Graminae pollen al
41	8	5.8	12	19 AAW76465	Graminae pollen al
42	8	5.8	12	19 AAW76466	Graminae pollen al
43	8	5.8	303	16 AAR71507	Dac gv (clone 259)
44	7	5.1	12	19 AAW76486	Graminae pollen al
45	7	5.1	12	19 AAW76487	Graminae pollen al
46	7	5.1	12	19 AAW76453	Graminae pollen al
47	7	5.1	20	16 AAR71520	LPX-13, peptide f
48	7	5.1	116	13 AAR27358	Sequence of a poly
49	7	5.1	118	13 AAR27359	Sequence of a poly
50	7	5.1	256	20 AAY35492	Chlamydia pneumoni

ALIGNMENTS

RESULT 1
ID AAY25640
ID AAY25640 standard; protein; 138 AA.
AC AAY25640;
XX
XX
DT 30-SEP-1999 (first entry)
XX
DE Phleum sp. allergen Phl p 6 protein fragment #5.
XX

KW Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; insect; stinging;
KW Chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
OS Phleum sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-GB00080.
XX
PR 21-SEP-1998; 98GB-0020474.
PR 09-JAN-1998; 98GB-0000445.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Desensitizing patients to polypeptide allergens

Example 6; Page 65; 117pp; English.

This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, cockroach, beetle, bee moth larvae, mealworm, cockroach, larvae of Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 6 allergen.

Sequence 57 AA;

Query Match 41.3%; Score 57; DB 20; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.3e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 SKAPQLVPKIDVYNAAYNAADHAAPEDKYEAFVLFHSEALHIITAGTPEVHAVKPGA 138
|||||
Db 1 skapqlvpkidevynaaynaadhaapedkyeafvlfhsealhiiagtpevhavkpga 57

RESULT 6
AAV25639
ID AAY25639 standard; protein; 106 AA.
AC AAY25639;
DT 30-SEP-1999 (first entry)
DE Phleum sp. allergen Phl p 6 protein fragment #4.
XX Major histocompatibility complex; class II; desensitizing; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX Phleum sp.
XX WO9934826-A1.
PN 15-JUL-1999.
XX 11-JAN-1999; 99WO-GB00080.
XX 21-SEP-1998; 98GB-0020474.
PR 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Kay AB, Larche M;
PI WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
PT Example 6; Page 66; 117pp; English.
PS This invention describes a novel method of desensitizing a patient to a
CC

polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, cockroach, beetle, bee moth larvae, mealworm, cockroach, larvae of Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 6 allergen.

Sequence 106 AA;

Query Match 41.3%; Score 57; DB 20; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.5e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 EAAFTVSSKRNLDADVSKAPQLVPKIDVYNAAYNAADHAAPEDKYEAFVLFHSEAL 122
|||||
Db 34 eaaftvsskrlnadavskapqlvpkidevynaaynaadhaapedkyeafvlfhseal 90

RESULT 7
AAW76447
ID AAW76447 standard; protein; 137 AA.
XX AC AAW76447;
XX DT 11-DEC-1998 (first entry)
XX Graminae pollen allergen Phl p 5b protein variant DM2.
DE Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
KW epitope; immunotherapy; allergy; hypersensitisation.
KW Graminae.
OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 49 /label= D49L
FT /note= "Wild-type Asp is replaced with Leu"
FT Misc-difference 50 /label= K50A
FT /note= "Wild-type Lys is replaced with Ala"
FT Misc-difference 50...51 /note= "Site of 128 amino acid deletion compared with wild-type sequence"
FT DE19713001-A1.
PN 01-OCT-1998.
XX 27-MAR-1997; 97DE-1013001.
XX 27-MAR-1997; 97DE-1013001.
XX (MERE) MERCK PATENT GMBH.
XX Becker W, Bufer A, Cromwell O, Fiebig H, Jaeger L;
PI Kahlert H, Mueller W, Schramm G, Stuewe H;
XX WPI; 1998-522170/45.
XX Modified recombinant allergens - useful for immuno-therapy of
PT allergies
XX

PS Example 3; Page 6; 31pp; German.
XX This sequence is DM2, a variant of a natural pollen allergen which has a
CC region deleted from amino acid 51 to amino acid 178 of the wild-type
CC Phi p 5b protein represented in AAW76442. This allergen is used in a
CC method which results in the reduction or elimination of reactivity of
CC the modified grass pollen allergens with IgE antibodies while their
CC reactivity with T cells is retained. The genes for the allergens are
CC modified so that the encoded polypeptides have one or more amino acid
CC substitutions, deletions and/or additions. The dominant T-cell epitopes
CC of the allergens are not genetically altered. Such allergens have
CC applications in the immunotherapy of allergies e.g. hyposensitisation.
XX Sequence 137 AA;
SQ

Query Match 10.9%; Score 15; DB 19; Length 137;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDIN 43
Db 18 gkatteeqklliedin 32
|||||

RESULT 8
AAW76446
ID AAW76446 standard; protein; 182 AA.
AC AAW76446;
XX
XX 11-DEC-1998 (first entry)
XX Graminae pollen allergen Phi p 5b protein variant DM1.
XX Pollen; allergen; Phi p 5b; IgE; antibody; grass; reactivity; T cell;
KW epitope; immunotherapy; allergy; hyposensitisation.
XX Graminae.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 49 /label= D49L
FT /note= "Wild-type Asp is replaced with Leu"
FT Misc-difference 49..50
FT /note= "Site of 83 amino acid deletion compared
FT with wild-type sequence"
XX
XX DE19713001-Al.
XX
XX 01-OCT-1998.
XX
XX 27-MAR-1997; 97DE-1013001.
XX
XX 27-MAR-1997; 97DE-1013001.
XX (MERE) MERCK PATENT GMBH.
XX
XX Becker W, Bufer A, Cromwell O, Fiebig H, Jaeger L;
PI Kahlert H, Mueller W, Schramm G, Stuewe H;
PI
XX WPI; 1998-522170/45.
XX
XX Modified recombinant allergens - useful for immuno-therapy of
PT allergies
PT
XX Example 3; Page 6; 31pp; German.
XX This sequence is DM1, a variant of a natural pollen allergen which has a
CC region deleted from amino acid 50 to amino acid 132 of the wild-type
CC Phi p 5b protein represented in AAW76442. This allergen is used in a
CC method which results in the reduction or elimination of reactivity of

CC the modified grass pollen allergens with IgE antibodies while their
CC reactivity with T cells is retained. The genes for the allergens are
CC modified so that the encoded polypeptides have one or more amino acid
CC substitutions, deletions and/or additions. The dominant T-cell epitopes
CC of the allergens are not genetically altered. Such allergens have
CC applications in the immunotherapy of allergies e.g. hyposensitisation.
XX Sequence 182 AA;
SQ

Query Match 10.9%; Score 15; DB 19; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDIN 43
Db 18 gkatteeqklliedin 32
|||||

RESULT 9
AAW76448
ID AAW76448 standard; protein; 241 AA.
XX
XX AAW76448;
XX
XX 11-DEC-1998 (first entry)
XX Graminae pollen allergen Phi p 5b protein variant DM3.
XX Pollen; allergen; Phi p 5b; IgE; antibody; grass; reactivity; T cell;
KW epitope; immunotherapy; allergy; hyposensitisation.
XX Graminae.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 220 /label= A220T
FT /note= "Wild-type Ala is replaced with Thr"
FT Misc-difference 153..154
FT /note= "Site of 25 amino acid deletion compared
FT with wild-type sequence"
XX
XX DE19713001-Al.
XX
XX 01-OCT-1998.
XX
XX 27-MAR-1997; 97DE-1013001.
XX
XX 27-MAR-1997; 97DE-1013001.
XX (MERE) MERCK PATENT GMBH.
XX
XX Becker W, Bufer A, Cromwell O, Fiebig H, Jaeger L;
PI Kahlert H, Mueller W, Schramm G, Stuewe H;
PI
XX WPI; 1998-522170/45.
XX
XX Modified recombinant allergens - useful for immuno-therapy of
PT allergies
PT
XX Example 3; Page 7; 31pp; German.
XX This sequence is DM3, a variant of a natural pollen allergen which has a
CC region deleted from amino acid 154 to amino acid 177 of the wild-type
CC Phi p 5b protein represented in AAW76442. This allergen is used in a
CC method which results in the reduction or elimination of reactivity of
CC the modified grass pollen allergens with IgE antibodies while their
CC reactivity with T cells is retained. The genes for the allergens are
CC modified so that the encoded polypeptides have one or more amino acid
CC substitutions, deletions and/or additions. The dominant T-cell epitopes
CC of the allergens are not genetically altered. Such allergens have
CC applications in the immunotherapy of allergies e.g. hyposensitisation.

```

XX      SQ      Sequence      241 AA;
Query Match      10.9%; Score 15; DB 19; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29      GKATTEQKLIEDIN 43
Db      18      gkatteeqklliedin 32
|||||

RESULT 10
AAW76442
ID      AAW76442 standard; protein; 265 AA.
XX
AC      AAW76442;
XX
DT      11-DEC-1998 (first entry)
XX
DE      Graminae pollen allergen Phl p 5b protein.
XX
KW      Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
KW      epitope; immunotherapy; allergy; hyposensitisation.
XX
OS      Graminae.
XX
PN      DE19713001-Al.
PD      01-OCT-1998.
XX
PF      27-MAR-1997; 97DE-1013001.
XX
PR      27-MAR-1997; 97DE-1013001.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Becker W, Bufo A, Cromwell O, Fiebig H, Jaeger L;
PI      Kahlert H, Mueller W, Schramm G, Stuewe H;
XX
WPI; 1998-522170/45.
XX
Modified recombinant allergens - useful for immuno-therapy of
allergies
XX
Example 1; Page 3; 3lpp; German.
XX
This sequence is a natural pollen allergen, Phl p 5b, isolated from
Graminae species. This allergen can be modified and the reactivity of
the modified allergens with IgE antibodies to grass pollen allergens
is reduced or eliminated while their reactivity with T cells is
retained. The genes for the allergens are modified so that the encoded
polypeptides have one or more amino acid substitutions, deletions
and/or additions. The dominant T-cell epitopes of the allergens are
not genetically altered. Such allergens have applications in the
immunotherapy of allergies e.g. hyposensitisation.
XX
SQ      Sequence      265 AA;

Query Match      10.9%; Score 15; DB 19; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29      GKATTEQKLIEDIN 43
Db      18      gkatteeqklliedin 32
|||||

RESULT 11
AAW76444
ID      AAW76444 standard; protein; 265 AA.
XX
AC      AAW76444;
XX
DT      11-DEC-1998 (first entry)
XX
DE      Graminae pollen allergen Phl p 5b protein variant PM3.
XX
KW      Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
KW      epitope; immunotherapy; allergy; hyposensitisation.
XX
OS      Graminae.
XX
PN      DE19713001-Al.
PD      01-OCT-1998.
XX
PF      27-MAR-1997; 97DE-1013001.
XX
PR      27-MAR-1997; 97DE-1013001.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Becker W, Bufo A, Cromwell O, Fiebig H, Jaeger L;
PI      Kahlert H, Mueller W, Schramm G, Stuewe H;
XX
WPI; 1998-522170/45.
XX
Modified recombinant allergens - useful for immuno-therapy of
allergies
XX
Example 2; Page 5; 3lpp; German.
XX
This sequence is PM2, a variant of a natural pollen allergen constructed
from the wild-type Phl p 5b sequence represented in AAW76442, isolated
from Graminae species. This allergen is used in a method which results in
the reduction or elimination of reactivity of the modified grass pollen
allergens with IgE antibodies while their reactivity with T cells is
retained. The genes for the allergens are modified so that the encoded
polypeptides have one or more amino acid substitutions, deletions and/or
additions. The dominant T-cell epitopes of the allergens are not
genetically altered. Such allergens have applications in the
immunotherapy of allergies e.g. hyposensitisation.
XX
SQ      Sequence      265 AA;

Query Match      10.9%; Score 15; DB 19; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29      GKATTEQKLIEDIN 43
Db      18      gkatteeqklliedin 32
|||||

RESULT 12
AAW76445
ID      AAW76445 standard; protein; 265 AA.
XX
AC      AAW76445;
XX
DT      11-DEC-1998 (first entry)
XX
DE      Graminae pollen allergen Phl p 5b protein variant PM3.

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XX      AC      AAW76444;
XX
DT      11-DEC-1998 (first entry)
XX
DE      Graminae pollen allergen Phl p 5b protein variant PM2.
XX
KW      Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
KW      epitope; immunotherapy; allergy; hyposensitisation.
XX
OS      Graminae.
XX
PN      DE19713001-Al.
PD      01-OCT-1998.
XX
PF      27-MAR-1997; 97DE-1013001.
XX
PR      27-MAR-1997; 97DE-1013001.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Becker W, Bufo A, Cromwell O, Fiebig H, Jaeger L;
PI      Kahlert H, Mueller W, Schramm G, Stuewe H;
XX
WPI; 1998-522170/45.
XX
Modified recombinant allergens - useful for immuno-therapy of
allergies
XX
Example 2; Page 5; 3lpp; German.
XX
This sequence is PM2, a variant of a natural pollen allergen constructed
from the wild-type Phl p 5b sequence represented in AAW76442, isolated
from Graminae species. This allergen is used in a method which results in
the reduction or elimination of reactivity of the modified grass pollen
allergens with IgE antibodies while their reactivity with T cells is
retained. The genes for the allergens are modified so that the encoded
polypeptides have one or more amino acid substitutions, deletions and/or
additions. The dominant T-cell epitopes of the allergens are not
genetically altered. Such allergens have applications in the
immunotherapy of allergies e.g. hyposensitisation.
XX
SQ      Sequence      265 AA;

Query Match      10.9%; Score 15; DB 19; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29      GKATTEQKLIEDIN 43
Db      18      gkatteeqklliedin 32
|||||

RESULT 12
AAW76445
ID      AAW76445 standard; protein; 265 AA.
XX
AC      AAW76445;
XX
DT      11-DEC-1998 (first entry)
XX
DE      Graminae pollen allergen Phl p 5b protein variant PM3.

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XX Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
KW epitope; immunotherapy; allergy; hyposensitisation.
XX
XX Graminae.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 13
FT /label= A13C
FT /note= "Wild-type Ala is replaced by Cys"
XX
XX DEL9713001-AL.
XX
XX 01-OCT-1998;
XX
XX 27-MAR-1997; 97DE-1013001.
XX
XX 27-MAR-1997; 97DE-1013001.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Becker W, Bufo A, Cromwell O, Fiebig H, Jaeger L;
PI Kahlert H, Mueller W, Schramm G, Stuewe H;
XX
XX WPI; 1998-522170/45.
XX
XX Modified recombinant allergens - useful for immuno-therapy of
PT allergies
XX
XX Example 2; Page 6; 31pp; German.
XX
XX This sequence is PM3, a variant of a natural pollen allergen constructed
CC from the wild-type Phl p 5b sequence represented in AAW76442, isolated
CC from Graminae species. This allergen is used in a method which results in
CC the reduction or elimination of reactivity of the modified grass pollen
CC allergens with IgE antibodies while their reactivity with T cells is
CC retained. The genes for the allergens are modified so that the encoded
CC polypeptides have one or more amino acid substitutions, deletions and/or
CC additions. The dominant T-cell epitopes of the allergens are not
CC genetically altered. Such allergens have applications in the
CC immunotherapy of allergies e.g. hyposensitisation.
XX
XX Sequence 265 AA;

Query Match 10.9%; Score 15; DB 19; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDIN 43
Db 18 gkateeekqliedin 32

RESULT 13
AAAY25621
ID AAY25621 standard; protein; 265 AA.
XX
XX AAY25621;
XX
XX 30-SEP-1999 (first entry)
XX
XX Phleum sp. allergen Phl p 5 protein fragment #5.
XX
XX Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
XX Phleum sp.
OS

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XX WO9934826-A1
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-CB00080.
XX
XX 21-SEP-1998; 98GB-0020474.
XX 09-JAN-1998; 98GB-0000445.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Kay AB, Larche M;
XX
XX WPI; 1999-458255/38.
XX
XX Desensitizing patients to polypeptide allergens
XX
XX Example 6; Page 61; 117pp; English.
XX
XX This invention describes a novel method of desensitizing a patient to a
CC polypeptide allergen and comprises administering to the patient a peptide
CC derived from the allergen where restriction to a MHC Class II molecule
CC possessed by the patient can be demonstrated for the peptide and the
CC peptide is able to induce a late phase response in an individual who
CC possesses the MHC Class II molecule. The methods can be used for
CC desensitising patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chiromidae (non-biting midges), spiders and mites, housefly, fruit
CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents a Phleum sp. (Timothy grass) Phl p 5 allergen.
XX
XX Sequence 265 AA;

Query Match 10.9%; Score 15; DB 20; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDIN 43
Db 18 gkateeekqliedin 32

RESULT 14
AAAY25628
ID AAY25628 standard; protein; 280 AA.
XX
XX AAY25628;
XX
XX 30-SEP-1999 (first entry)
XX
XX Phleum sp. allergen Phl p 5b protein fragment #3.
XX
XX Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
XX Phleum sp.
OS
XX WO9934826-A1.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-CB00080.
XX

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PS Example 6; Page 63; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of tenbriol molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5 allergen.

XX Sequence 281 AA;

Query Match 10.9%; Score 15; DB 20; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIEDIN 43
Db 34 gkateeekliedlin 48
|||||

RESULT 17
AAV25625
ID AAV25625 standard; protein; 284 AA.

XX AC AAV25625;

XX DT 30-SEP-1999 (first entry)

XX DE Phleum sp. allergen Phl p 5b protein fragment #2.

XX KW Major histocompatibility complex; class II; desensitising; human;
allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX OS Phleum sp.

XX PN WO9934826-A1.

XX PD 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-GB00080.

XX PR 21-SEP-1998; 98GB-0020474.

XX PR 09-JAN-1998; 98GB-0000445.

XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Kay AB, Larche M;

XX PS WPI; 1999-458255/38.

XX Desensitizing patients to polypeptide allergens

XX Example 6; Page 62; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the

CC peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of tenbriol molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5b allergen.

XX Sequence 284 AA;

Query Match 10.9%; Score 15; DB 20; Length 284;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIEDIN 43
Db 37 gkateeekliedlin 51
|||||

RESULT 18
AAV25617
ID AAV25617 standard; protein; 284 AA.

XX AC AAV25617;

XX DT 30-SEP-1999 (first entry)

XX DE Phleum sp. allergen Phl p 5b protein fragment #1.

XX KW Major histocompatibility complex; class II; desensitising; human;
allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX OS Phleum sp.

XX PN WO9934826-A1.

XX PD 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-GB00080.

XX PR 21-SEP-1998; 98GB-0020474.

XX PR 09-JAN-1998; 98GB-0000445.

XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Kay AB, Larche M;

XX PS WPI; 1999-458255/38.

XX Desensitizing patients to polypeptide allergens

XX Example 6; Page 60; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,

CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents a Phleum sp. (Timothy grass) Phl p 5b allergen.
 XX
 SQ Sequence 284 AA;
 Query Match 10.9%; Score 15; DB 20; Length 284;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 GRATTEEQLIEDIN 43
 DB 37 gkateeqliedin 51
 RESULT 19
 AAY25619
 ID AAY25619 standard; protein; 287 AA.
 XX
 AC AAY25619;
 XX
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Phleum sp. allergen Phl p 5 protein fragment #3.
 XX
 KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
 XX
 OS Phleum sp.
 XX
 PN WO934826-A1.
 XX
 PD 15-JUL-1999.
 XX
 XX 11-JAN-1999; 99WO-GB000080.
 PF
 PR 21-SEP-1998; 98GB-0020474.
 PR 09-JAN-1998; 98GB-0000445.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Kay AB, Larche M;
 PI
 DR WPI; 1999-458255/38.
 XX
 XX Desensitizing patients to polypeptide allergens
 PS
 PS Example 6; Page 60; 117pp; English.
 XX
 CC This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who
 CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitizing patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents a Phleum sp. (Timothy grass) Phl p 5 allergen.

XX
 SQ Sequence 287 AA;
 Query Match 10.9%; Score 15; DB 20; Length 287;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 GRATTEEQLIEDIN 43
 DB 43 gkateeqliedin 57
 RESULT 20
 AAY25620
 ID AAY25620 standard; protein; 290 AA.
 XX
 AC AAY25620;
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Phleum sp. allergen Phl p 5 protein fragment #4.
 XX
 KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
 XX
 OS Phleum sp.
 XX
 PN WO934826-A1.
 XX
 PD 15-JUL-1999.
 XX
 XX 11-JAN-1999; 99WO-GB000080.
 PF
 PR 21-SEP-1998; 98GB-0020474.
 PR 09-JAN-1998; 98GB-0000445.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Kay AB, Larche M;
 PI
 DR WPI; 1999-458255/38.
 XX
 XX Desensitizing patients to polypeptide allergens
 PS
 PS Example 6; Page 61; 117pp; English.
 XX
 CC This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who
 CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitizing patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents a Phleum sp. (Timothy grass) Phl p 5 allergen.
 XX
 SQ Sequence 290 AA;
 Query Match 10.9%; Score 15; DB 20; Length 290;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDIN 43
| | | | | | | | | | | |
Db 43 gkatteeqklliedin 57

RESULT 21

AAV25622
ID AAY25622 standard; protein; 295 AA.

XX AC AAY25622;

XX DT 30-SEP-1999 (first entry)

XX DE Phleum sp. allergen Phl p 5 protein fragment #6.

XX KW Major histocompatibility complex; class II; desensitising; human;
XX KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
XX KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX OS Phleum sp.

XX PN WO9934826-A1.

XX PD 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-GB000080.

XX PR 21-SEP-1998; 98GB-0020474.

XX PR 09-JAN-1998; 98GB-0000445.

XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Kay AB, Larche M;

XX PI WPI; 1999-458255/38.

XX PT Desensitizing patients to polypeptide allergens

XX PS Example 6; Page 61; 117pp; English.

XX CC This invention describes a novel method of desensitizing a patient to a
XX CC polypeptide allergen and comprises administering to the patient a peptide
XX CC derived from the allergen where restriction to a MHC Class II molecule
XX CC possessed by the patient can be demonstrated for the peptide and the
XX CC peptide is able to induce a late phase response in an individual who
XX CC possesses the MHC Class II molecule. The methods can be used for
XX CC desensitising patients to allergens present in e.g. grass, tree and weed
XX CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX CC produce immunological vaccines which may be used to prevent and/or treat
XX CC conditions involving hypersensitivity to allergens. This sequence
XX CC represents a Phleum sp. (Timothy grass) Phl p 5 allergen.

XX SQ Sequence 295 AA;

Query Match 10.9%; Score 15; DB 20; Length 295;

Best Local Similarity 100.0%; Pred. No. 4e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDIN 43

| | | | | | | | | | | |

Db 48 gkatteeqklliedin 62

RESULT 22

AAW76443

ID AAW76443 standard; protein; 265 AA.

XX AC AAW76443;

XX DT 11-DEC-1998 (first entry)

XX DE Graminae pollen allergen Phl p 5b protein variant PM1.

XX KW Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
XX KW epitope; immunotherapy; allergy; hyposensitisation.

XX OS Graminae.

XX FH Key Location/Qualifiers

XX FT Misc-difference 32

XX FT /label= N32D

XX FT /note= "Wild-type Asn is replaced by Asp"

XX FT Misc-difference 49

XX FT /label= D49L

XX FT /note= "Wild-type Asp is replaced by Leu"

XX FT Misc-difference 50

XX FT /label= K50A

XX FT /note= "Wild-type Lys is replaced by Ala"

XX PN DE19713001-A1.

XX PD 01-OCT-1998.

XX PF 27-MAR-1997; 97DE-1013001.

XX PR 27-MAR-1997; 97DE-1013001.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Becker W, Bufer A, Cromwell O, Fiebig H, Jaeger L;

XX PI Kahler H, Mueller W, Schramm G, Stuewe H;

XX DR WPI; 1998-522170/45.

XX PT Modified recombinant allergens - useful for immuno-therapy of
XX PT allergies
XX PS Example 2; Page 5; 31pp; German.

XX CC This sequence is PM1, a variant of a natural pollen allergen,
XX CC constructed from the wild-type Phl p 5b sequence represented in AAW76442,
XX CC isolated from Graminae species. This allergen is used in a method which
XX CC results in the reduction or elimination of reactivity of the modified
XX CC grass pollen allergens with IgE antibodies while their reactivity with T
XX CC cells is retained. The genes for the allergens are modified so that the
XX CC encoded polypeptides have one or more amino acid substitutions, deletions
XX CC and/or additions. The dominant T-cell epitopes of the allergens are not
XX CC genetically altered. Such allergens have applications in the
XX CC immunotherapy of allergies e.g. hyposensitisation.

XX SQ Sequence 265 AA;

Query Match 10.1%; Score 14; DB 19; Length 265;

Best Local Similarity 100.0%; Pred. No. 3.7e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GKATTEQKLIEDI 42

| | | | | | | | | | | |

Db 18 gkatteeqklliedi 31

RESULT 23

AAW76455

ID AAW76455 standard; peptide; 12 AA.

```
XX AC AAW76455;
XX DT 11-DEC-1998 (first entry)
XX DE Graminae pollen allergen Phl p 5b peptide fragment #7.
XX KW Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell;
KW epitope; immunotherapy; allergy; hyposensitisation.
XX OS Graminae.
XX PN DE19713001-A1.
XX PD 01-OCT-1998.
XX PF 27-MAR-1997; 97DE-1013001.
XX PR 27-MAR-1997; 97DE-1013001.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Becker W, Bufo A, Cromwell O, Fiebig H, Jaeger L;
PI Kahler H, Mueller W, Schramm G, Stuewe H;
XX WPI; 1998-522170/45.
XX DR Modified recombinant allergens - useful for immuno-therapy of
XX PT allergies
XX PS Example 1; Page 12; 31pp; German.
XX CC AAW76449-W76534 are peptide fragments of a natural pollen allergen,
XX CC Phl p 5b, isolated from Graminae species. This allergen can be modified
XX CC and the reactivity of the modified allergens with IgE antibodies to
XX CC grass pollen allergens is reduced or eliminated while their reactivity
XX CC with T cells is retained. The genes for the allergens are modified so
XX CC that the encoded polypeptides have one or more amino acid substitutions,
XX CC deletions and/or additions. The dominant T-cell epitopes of the
XX CC allergens are not genetically altered. Such allergens have applications
XX CC in the immunotherapy of allergies e.g. hyposensitisation.
XX SQ Sequence 12 AA;

Query Match 8.7%; Score 12; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 KATTEQKLIED 41
Db 1 kateeekqlied 12

RESULT 24
AAAY25630
ID AAY25630 standard; protein; 257 AA.
XX AC AAY25630;
XX DT 30-SEP-1999 (first entry)
XX DE Phleum sp. allergen Phl p 5 protein fragment #11.
XX KW Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX OS Phleum sp.
XX PF 11-JAN-1999; 99WO-GB000080.
XX
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PN WO9934826-A1.
XX 15-JUL-1999.
XX PF 11-JAN-1999; 99WO-GB000080.
XX PR 21-SEP-1998; 98GB-0020474.
XX PR 09-JAN-1998; 98GB-0000445.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Kay AB, Larche M;
XX WPI; 1999-458255/38.
XX DR Desensitizing patients to polypeptide allergens
XX PT
XX PS Example 6; Page 64; 117pp; English.
XX CC This invention describes a novel method of desensitizing a patient to a
XX CC polypeptide allergen and comprises administering to the patient a peptide
XX CC derived from the allergen where restriction to a MHC Class II molecule
XX CC possessed by the patient can be demonstrated for the peptide and the
XX CC peptide is able to induce a late phase response in an individual who
XX CC possesses the MHC Class II molecule. The methods can be used for
XX CC desensitizing patients to allergens present in e.g. grass, tree and weed
XX CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX CC tenbribo molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX CC produce immunological vaccines which may be used to prevent and/or treat
XX CC conditions involving hypersensitivity to allergens. This sequence
XX CC represents a Phleum sp. (Timothy grass) Phl p 5 allergen.
XX SQ Sequence 257 AA;

Query Match 8.7%; Score 12; DB 20; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEEQKLIIE 40
Db 5 gkateeekqliie 16

RESULT 25
AAAY25615
ID AAY25615 standard; protein; 276 AA.
XX AC AAY25615;
XX DT 30-SEP-1999 (first entry)
XX DE Phleum sp. allergen Phl p 5 protein fragment #1.
XX KW Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX OS Phleum sp.
XX PN WO9934826-A1.
XX PR 15-JUL-1999.
XX PF 11-JAN-1999; 99WO-GB000080.
XX
```

PR 21-SEP-1998; 98GB-0020474.
PR 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Kay AB, Larche M;
XX WPI; 1999-458255/38.
DR Desensitizing patients to polypeptide allergens
XX Example 6; Page 59; 117pp; English.
XX This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5 allergen.
XX Sequence 276 AA;
SQ

Query Match 8.7%; Score 12; DB 20; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GRATTEEQKLIE 40
DB 21 gkatteeqklie 32
IIIIIIIIII

RESULT 26
AAY25616
ID AAY25616 standard; protein; 276 AA.
AC AAY25616;
XX
XX 30-SEP-1999 (first entry)
XX Phleum sp. allergen Phl p 5 protein fragment #2.
XX Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX Phleum sp.
OS
XX
XX WO9934826-A1.
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-GB000080.
XX
XX 21-SEP-1998; 98GB-0020474.
XX 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Kay AB, Larche M;
XX WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
XX Example 6; Page 52; 117pp; English.

XX WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
XX Example 6; Page 59-60; 117pp; English.
XX This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5 allergen.
XX Sequence 276 AA;
SQ

Query Match 8.7%; Score 12; DB 20; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GRATTEEQKLIE 40
DB 21 gkatteeqklie 32
IIIIIIIIII

RESULT 27
AAY25624
ID AAY25624 standard; protein; 276 AA.
XX
XX AAY25624;
XX
XX 30-SEP-1999 (first entry)
XX Phleum sp. allergen Phl p 5 protein fragment #8.
XX Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX Phleum sp.
OS
XX
XX WO9934826-A1.
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-GB000080.
XX
XX 21-SEP-1998; 98GB-0020474.
XX 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Kay AB, Larche M;
XX WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
XX Example 6; Page 62; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who
 CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitizing patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC tenbriol molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents a Phleum sp. (Timothy grass) Phl p 5 allergen.
 XX
 SQ Sequence 276 AA;

Query Match 8.7%; Score 12; DB 20; Length 276;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIE 40
 DB 21 gkatteeqklie 32
 |||||

RESULT 28
 AAY25633
 ID AAY25633 standard; protein; 285 AA.
 AC AAY25633;
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Phleum sp. allergen Phl p 5a protein fragment #3.
 XX
 KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
 XX
 OS Phleum sp.
 XX
 PN WO9934826-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 11-JAN-1999; 99WO-GB000080.
 XX
 PR 21-SEP-1998; 98GB-0020474.
 XX
 PR 09-JAN-1998; 98GB-0000445.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Kay AB, Larche M;
 XX
 PS WPI; 1999-458255/38.
 XX
 PT Desensitizing patients to polypeptide allergens
 XX
 PS Example 6; Page 64-65; 117pp; English.
 XX
 CC This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who

CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitizing patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC tenbriol molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents a Phleum sp. (timothy grass) Phl p 5a allergen.
 XX
 SQ Sequence 285 AA;

Query Match 8.7%; Score 12; DB 20; Length 285;
 Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIE 40
 DB 32 gkatteeqklie 43
 |||||

RESULT 29
 AAY25626
 ID AAY25626 standard; protein; 286 AA.
 AC AAY25626;
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Phleum sp. allergen Phl p 5a protein fragment #2.
 XX
 KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
 XX
 OS Phleum sp.
 XX
 PN WO9934826-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 11-JAN-1999; 99WO-GB000080.
 XX
 PR 21-SEP-1998; 98GB-0020474.
 XX
 PR 09-JAN-1998; 98GB-0000445.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Kay AB, Larche M;
 XX
 PS WPI; 1999-458255/38.
 XX
 PT Desensitizing patients to polypeptide allergens
 XX
 PS Example 6; Page 62-63; 117pp; English.
 XX
 CC This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who
 CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitizing patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of

CC Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents a Phleum sp. (timothy grass) Phl p 5a allergen.
XX
SQ Sequence 286 AA;

Query Match 8.7%; Score 12; DB 20; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GKATTEQKLIIE 40
Db 32 gkatteeqkllie 43

RESULT 30
AAAY25618
ID AAY25618 standard; protein; 286 AA.
XX AC AAY25618;
XX 30-SEP-1999 (first entry)
DT Phleum sp. allergen Phl p 5a protein fragment #1.
DE Major histocompatibility complex; class II; desensitising; human;
XX allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX Phleum sp.
OS W09934826-A1.
XX 15-JUL-1999.
XX 11-JAN-1999; 99WO-GB00080.
XX 21-SEP-1998; 98GB-0020474.
PR 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Kay AB, Larche M;
XX WPI; 1999-458255/38.
XX Desensitizing patients to polypeptide allergens
PT
XX Example 6; Page 60; 117pp; English.
XX This invention describes a novel method of desensitizing a patient to a
CC polypeptide allergen and comprises administering to the patient a peptide
CC derived from the allergen where restriction to a MHC Class II molecule
CC possessed by the patient can be demonstrated for the peptide and the
CC peptide is able to induce a late phase response in an individual who
CC possesses the MHC class II molecule. The methods can be used for
CC desensitising patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents a Phleum sp. (timothy grass) Phl p 5a allergen.
XX

SQ Sequence 286 AA;
Query Match 8.7%; Score 12; DB 20; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GKATTEQKLIIE 40
Db 32 gkatteeqkllie 43
Search completed: November 19, 2001, 13:09:24
Job time: 30 sec

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OM protein - protein search, using sw model

Run on: November 19, 2001, 13:09:30 ; Search time 22.52 Seconds
(without alignments)
810.750 Million cell updates/sec

Title: CAA76556
Perfect score: 138
Sequence: 1 MAHKFWAMFLAVAVLGL.....SEALHIAGTPEVHAVKPGA 138

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
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Post-processing: Listing first 50 summaries

Database : SPTREMBL_16.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				%					
Result No.	Score	Query Match	Length	DB ID	Description				
1	138	100.0	138	10	O65868				
2	57	41.3	106	10	O65869				
3	17	12.3	264	10	O23972				
4	15	10.9	265	10	OQSR80				
5	15	10.9	281	10	P93466				
6	15	10.9	287	10	O81344				
7	15	10.9	290	10	O81343				
8	15	10.9	295	10	O81342				
9	12	8.7	276	10	O65318				
10	12	8.7	276	10	O65319				
11	12	8.7	276	10	O65320				
12	12	8.7	276	10	O65321				
13	12	8.7	276	10	P93467				
14	12	8.7	312	10	O40960				
15	12	8.7	312	10	O81341				
16	10	7.2	240	10	O23971				
17	8	5.8	255	2	Q912R7				
18	8	5.8	443	10	O23824				
19	8	5.8	503	2	Q9PKB6				

Q9PKB6 chlamydia m

ALIGNMENTS

RESULT 1
O65868 ID O65868 PRELIMINARY; PRT; 138 AA.
AC O65868
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHL P6 ALLERGEN PRECURSOR.
OS PHL P6
GN Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C223 AND C146 AND C233, AND C121; TISSUE=POLLEN;
RA Vrtala S., Fischer S., Grote M., Vangelista L., Pastore A.,
RA Sperr W.R., Valent P., Reichelt R., Kraft D., Valenta R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y16955; CAA76556.1; -
DR EMBL; Y16960; CAA76561.1; -
DR EMBL; Y16959; CAA76560.1; -
DR EMBL; Y16958; CAA76559.1; -
DR Mendel; 29288; Phlpr;1486;29288.
DR InterPro; IPR002914; -
DR Pfam; PF01620; Pollen_allerg_2; 1.
KW Signal; Allergen.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 138 POTENTIAL.
SQ SEQUENCE 138 AA; 14601 MW; 6483AB8C91978F38 CRC64;

Query Match 100.0%; Score 138; DB 10; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.6e-131;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHKFWAMFLAVAVLGLATPTAEGGKATTEEQKLIEDINASFRAAMATTANVPAD 60

```
Db 1 MAHKFMVAMFLAVVVLGLATSTAGGKATTEQKLIEDINASFRAAMATTANVPAD 60
QY 61 KYTFFAAFTVSSKRNLADAVSKAPQLVPKLDVYNAAADHAAPEDKYFAFVLHFE 120
Db 61 KYTFFAAFTVSSKRNLADAVSKAPQLVPKLDVYNAAADHAAPEDKYFAFVLHFE 120
QY 121 ALHIIAGTPEVHAVKPGA 138
Db 121 ALHIIAGTPEVHAVKPGA 138

RESULT 2
ID O65869 PRELIMINARY; PRT; 106 AA.
AC O65869;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DE PHL P6 IGE BINDING FRAGMENT (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C171; TISSUE=POLLEN;
RA Vrtala S., Fischer S., Grote M., Vangelista L., Pastore A.,
RA Sperr W.R., Valent P., Reichelt R., Kraft D., Valenta R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y16957; CAA76556.1; -
DR Mendel; 29289; Phlpr; 1486; 29289.
DR InterPro; IPR002914; -
DR Pfam; PF01620; Pollen_allerg_2; 1.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11399 MW; 4693F59458E46565 CRC64;

Query Match 41.3%; Score 57; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 EAAFTVSSKRNLADAVSKAPQLVPKLDVYNAAADHAAPEDKYFAFVLHFEAL 122
Db 34 EAAFTVSSKRNLADAVSKAPQLVPKLDVYNAAADHAAPEDKYFAFVLHFEAL 90

RESULT 3
ID O23972 PRELIMINARY; PRT; 264 AA.
AC O23972;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DE GROUP V ALLERGEN (FRAGMENT).
GN 5.
OS Holcus lanatus (Velvet grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poae; Holcus.
OX NCBI_TaxID=29679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLCUS LANATUS; TISSUE=INFLORESCENCE;
RX MEDLINE=98181862; PubMed=9523689;
RA Schramm G., Bufer A., Petersen A., Schlaak M., Becker W.;
RT Molecular and immunological characterization of group V allergen
RL Isoforms from velvet grass pollen (Holcus lanatus).";
RL Eur. J. Biochem. 252:200-206(1998).
DR EMBL; Z97874; CAB10765.1; -
DR Mendel; 25604; Holla; 1486; 25604.
DR InterPro; IPR001778; -
DR InterPro; IPR002914; -
DR Pfam; PF01620; Pollen_allerg_2; 1.

Query Match 10.9%; Score 15; DB 10; Length 265;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIEDIN 43
Db 18 GKATTEQKLIEDIN 32

RESULT 5
ID P93466 PRELIMINARY; PRT; 281 AA.
AC P93466;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DE MAJOR ALLERGEN PHL P 5 PRECURSOR (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poae; Phleum.
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DR PRINTS; PR00833; POAALLERGEN.
FT NON_TER 1
SQ SEQUENCE 264 AA; 26216 MW; 3F9409429DC9337F CRC64;

Query Match 12.3%; Score 17; DB 10; Length 264;
Best Local Similarity 100.0%; Pred. No. 5.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ANVPPADKYKTFEAAFT 70
Db 42 ANVPPADKYKTFEAAFT 58

RESULT 4
ID Q9SBE0 PRELIMINARY; PRT; 265 AA.
AC Q9SBE0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE GROUP V ALLERGEN PHL P 5.0204 (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=POLLEN;
RX MEDLINE=97390090; PubMed=9249029;
RA Gehlhar K., Petersen A., Schramm G., Becker W.M., Schlaak M., Bufer A.;
RT "Investigation of different recombinant isoforms of grass group-V
allergens (timothy grass pollen) isolated by low-stringency cDNA
hybridization-antibody binding capacity and allergenic activity.";
RL Eur. J. Biochem. 247:217-223(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=POLLEN;
RA Gehlhar K., Bufer A., Petersen A., Schramm G., Becker W.M., Schlaak M.;
RT "Investigation of different recombinant isoforms of grass group-V
allergens of timothy grass (Phleum pratense).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF069472; AAC25996.1; -
DR InterPro; IPR00104; -
DR InterPro; IPR001778; -
DR InterPro; IPR002914; -
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00308; ANTIFREEZE1.
DR PRINTS; PR00833; POAALLERGEN.
FT NON_TER 1
SQ SEQUENCE 265 AA; 26210 MW; BA3442E684419DE4 CRC64;

Query Match 10.9%; Score 15; DB 10; Length 265;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLIEDIN 43
Db 18 GKATTEQKLIEDIN 32

RESULT 5
ID P93466 PRELIMINARY; PRT; 281 AA.
AC P93466;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DE MAJOR ALLERGEN PHL P 5 PRECURSOR (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poae; Phleum.
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Best Local Similarity 100.0%; Pred. No. 6e-07;		Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	29 GKATTEQKLIEDIN 43		
DB	43 GKATTEQKLIEDIN 57		
RESULT 7			
OB1343			
ID	OB1343	PRELIMINARY;	PRT; 290 AA.
AC	OB1343;		
DT	01-NOV-1998 (TREMBlrel. 08, Created)		
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)		
DT	01-MAY-2000 (TREMBlrel. 13, Last annotation update)		
DE	GROUP V ALLERGEN PHL P 5.0206 PRECURSOR.		
OS	Phleum pratense (Common timothy).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Pooideae; Phleum.		
OX	NCBI_TaxID=15957;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=POLLEN;		
RX	MEDLINE=97390090; PubMed=9249029;		
RA	Gehlhar K., Petersen A., Schramm G., Becker W.M., Schlaak M., Bufe A.;		
RT	"Investigation of different recombinant isoforms of grass group-V		
RT	allergens (timothy grass pollen) isolated by low-stringency cDNA		
RT	hybridization--antibody binding capacity and allergenic activity.";		
RL	Eur. J. Biochem. 247:217-223(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=POLLEN;		
RA	Gehlhar K., Bufe A., Petersen A., Schramm G., Becker W.M., Schlaak M.;		
RT	"Investigation of different recombinant isoforms of grass group-V		
RT	allergens of timothy grass (Phleum pratense).";		
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF069473; AAC25997.1; -		
DR	Mendel; 31983; Phlpr; 1486; 31983.		
DR	InterPro; IPR001778; -		
DR	InterPro; IPR002914; -		
DR	Pfam; PF01620; Pollen_allerg.2; 1.		
DR	PRINTS; PR00833; POALLERGEN.		
KW	Signal.		
FT	SIGNAL	1 25	POTENTIAL.
FT	CHAIN	26 290	GROUP V ALLERGEN PHL P 5.0206.
SQ	SEQUENCE	290 AA; 28829 MW; D5D37C2542C0CC40	CRC64;
Query Match 10.9%; Score 15; DB 10; Length 290;			
Best Local Similarity 100.0%; Pred. No. 6.1e-07;			
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	29 GKATTEQKLIEDIN 43		
DB	43 GKATTEQKLIEDIN 57		
RESULT 8			
OB1342			
ID	OB1342	PRELIMINARY;	PRT; 295 AA.
AC	OB1342;		
DT	01-NOV-1998 (TREMBlrel. 08, Created)		
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)		
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)		
DE	GROUP V ALLERGEN PHL P 5.0203 PRECURSOR (FRAGMENT).		
OS	Phleum pratense (Common timothy).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Pooideae; Phleum.		
OX	NCBI_TaxID=15957;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=POLLEN;		
RX	MEDLINE=97390090; PubMed=9249029;		

RESULT 10	
O65319	
ID O65319	PRELIMINARY;
AC O65319;	PRT; 276 AA.

RESULT 12
O65321
ID O65321 PRELIMINARY; PRT; 276 AA.

DT	01-AUG-1998 (TrEMBLrel. 07, Created)
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

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DE MAJOR ALLERGEN PHL P 5 (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RA Wissenbach M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF061069; AAC16528.1; -.
DR Mendel; 28990; Phlpr;1486;28990.
DR InterPro; IPR001778; -.
DR InterPro; IPR002914; -.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POALLERGEN.
FT NON_TER 1
SQ SEQUENCE 276 AA; 27709 MW; 07FC5F654E3697CB CRC64;

Query Match      8.7%; Score 12; DB 10; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLLIE 40
Db 21 GKATTEQKLLIE 32

RESULT 13
P93467
ID P93467 PRELIMINARY; PRT; 276 AA.
AC P93467;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MAJOR ALLERGEN PHL P 5 (FRAGMENT).
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=POACEAE;
RX MEDLINE=97390090; PubMed=9249029;
RA Gehlhar K., Petersen A., Schramm G., Becker W.M., Schlaak M., Bufer A.;
RT "Investigation of different recombinant isoforms of grass group-V
allergens (timothy grass pollen) isolated by low-stringency cDNA
hybridization--antibody binding capacity and allergenic activity.";
RL Eur. J. Biochem. 247:217-223(1997).
DR EMBL; Z82986; CAB05372.1; -.
DR Mendel; 9951; Phlpr;1486;9951.
DR InterPro; IPR001778; -.
DR InterPro; IPR002914; -.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POALLERGEN.
FT NON_TER 1
SQ SEQUENCE 276 AA; 27702 MW; DB128F78E72AF1F3 CRC64;

Query Match      8.7%; Score 12; DB 10; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLLIE 40
Db 21 GKATTEQKLLIE 32

RESULT 14
Q40960
ID Q40960 PRELIMINARY; PRT; 312 AA.
AC Q40960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PHLPS PRECURSOR.
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RA Vrtala S., Sperr W.R., Reimtzner I., Van Ree R., Laffer S.,
RA Mueller W.D., Valent P., Lechner K., Rumpold H., Kraft D.,
RA Scheiner O., Valenta R.;
RL J. Immunol. 0:0-0(0).
DR EMBL; X74735; CAA52753.1; -.
DR Mendel; 9952; Phlpr;1486;9952.
DR InterPro; IPR001778; -.
DR InterPro; IPR002914; -.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POALLERGEN.
KW Signal; Allergen.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 312 POTENTIAL.
SQ SEQUENCE 312 AA; 31102 MW; BC94B13818CEE07F CRC64;

Query Match      8.7%; Score 12; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEQKLLIE 40
Db 57 GKATTEQKLLIE 68

RESULT 15
O81341
ID O81341 PRELIMINARY; PRT; 312 AA.
AC O81341;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GROUP V ALLERGEN PHL P 5.0103 PRECURSOR.
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=POLLEN;
RX MEDLINE=97390090; PubMed=9249029;
RA Gehlhar K., Petersen A., Schramm G., Becker W.M., Schlaak M., Bufer A.;
RT "Investigation of different recombinant isoforms of grass group-V
allergens (timothy grass pollen) isolated by low-stringency cDNA
hybridization--antibody binding capacity and allergenic activity.";
RL Eur. J. Biochem. 247:217-223(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=POLLEN;
RA Gehlhar K., Bufer A., Petersen A., Schramm G., Becker W.M., Schlaak M.;
RT "Investigation of different recombinant isoforms of grass group-V
allergens of timothy grass (Phleum pratense).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF069470; AAC25994.1; -.
DR Mendel; 31981; Phlpr;1486;31981.
DR InterPro; IPR001778; -.
DR InterPro; IPR002914; -.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POALLERGEN.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 312 GROUP V ALLERGEN PHL P 5.0103.
SQ SEQUENCE 312 AA; 31029 MW; E78C2872A6CE8F49 CRC64;

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Query Match 8.7%; Score 12; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GKATTEOKLIE 40
|||||
Db 57 GKATTEOKLIE 68

RESULT 16

O23971 PRELIMINARY; PRT; 240 AA.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GROUP V GRASS POLLEN ALLERGEN (FRAGMENT).
GN 5.02.
OS Holcus lanatus (Velvet grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Poaceae; Holcus.
OX NCBI_TaxID=29679;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-HOLCUS LANATUS; TISSUE=INFLORESCENCE;
RX MEDLINE=98181862; PubMed=9523689;
RA Schramm G., Bufo A., Petersen A., Schlaak M., Becker W.;
RT "Molecular and immunological characterization of group V allergen
isoforms from velvet grass pollen (Holcus lanatus).";
RL Eur. J. Biochem. 252:200-206(1998).
DR EMBL; Z97875; CAB10766.1; -;
DR Mendel; 25603; Holla; 1486; 25603.
DR InterPro; IPR001778; -;
DR InterPro; IPR002914; -;
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POALLERGEN.
FT NON_TER
FT 1
SQ SEQUENCE 240 AA; 24708 MW; AD232F202CF76C9F CRC64;

Query Match 7.2%; Score 10; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 VPPADKYKTF 65
|||||
Db 21 VPPADKYKTF 30

RESULT 17

ID Q912R7 PRELIMINARY; PRT; 255 AA.

AC Q912R7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROBABLE SHORT-CHAIN DEHYDROGENASE.
GN PA1828.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004609; AAG05217.1; -;
DR InterPro; IPR002198; -;
DR InterPro; IPR002347; -;
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PR00081; GDRDH.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
SQ SEQUENCE 255 AA; 26919 MW; D6CAD2D77EB726EC CRC64;

Query Match 5.8%; Score 8; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 TAEGGKAT 32
|||||
Db 56 TAEGGKAT 63

RESULT 18

O23824 PRELIMINARY; PRT; 443 AA.

AC O23824;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE FATTY ACID DESATURASE.
GN FAD7.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Panicoideae;
OC Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HONEY BANTUM;
RA Berberich T., Harada M., Sugawara K., Kodama H., Iba K., Kusano T.;
RL Plant Mol. Biol. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN=HONEY BANTUM;
RX MEDLINE=98145435; PubMed=9484441;
RA Berberich T., Harada M., Sugawara K., Kodama H., Iba K., Kusano T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
differential expression to temperature.";
RL Plant Mol. Biol. 36:297-306(1998).
DR EMBL; D63954; BAA22441.1; -;
DR EMBL; D63952; BAA22439.1; -;
DR Mendel; 24010; Zeama; 1208; 24010.
DR InterPro; IPR001225; -;
DR Pfam; PF00487; FA_desaturase; 1.
DR PRODOM; PD001081; -; 1.
SQ SEQUENCE 443 AA; 49437 MW; C9B41370CBB25D5D0 CRC64;

Query Match 5.8%; Score 8; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VAVVLGLA 21
|||||
Db 123 VAVVLGLA 130

RESULT 19

O9PKB6 PRELIMINARY; PRT; 503 AA.

ID O9PKB6
AC O9PKB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE NADH:UBIQUINONE OXIDOREDUCTASE, SUBUNIT B, PUTATIVE.
GN TC0550.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOPN / NIGG;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
  White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
  Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
  RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
  RA Eisen J., Fraser C.M.;
  RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
  pneumoniae AR39.";
  RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002323; AAF39389.1; -.
DR TIGR; TC0550; -.
SQ SEQUENCE 503 AA; 54968 MW; 6C9293E3842028AA CRC64;

Query Match 5.8%; Score 8; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TSPTAEGG 29
  |||||
Db 313 TSPTAEGG 320

RESULT 20
O68042
ID O68042 PRELIMINARY; PRT; 578 AA.
AC O68042;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DE TRANSMEMBRANE PROTEIN DHLC HOMOLOG.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
CC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003;
RX MEDLINE=97404404; PubMed=9256491;
RA Vleck C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.;
  RT "Sequence of a 189-kb segment of the chromosome of Rhodobacter
  capsulatus SB1003.";
  RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
DR EMBL; AF010496; AAC16128.1; -.
DR InterPro; IPR001734; -.
DR Pfam; PF00474; SSF; 1.
DR PROSITE; PS00456; NA_SOLUT_SYMP_1; 1.
DR PROSITE; PS02883; NA_SOLUT_SYMP_3; 1.
KW Transmembrane.
SQ SEQUENCE 578 AA; 60637 MW; 277C9134EE0894C5 CRC64;

Query Match 5.8%; Score 8; DB 2; Length 578;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VAVVLGLA 21
  |||||
Db 442 VAVVLGLA 449

RESULT 21
Q59019
ID Q59019 PRELIMINARY; PRT; 765 AA.
AC Q59019;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DE HYPOTHETICAL PROTEIN MJ1626.
GN MJ1626.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
  Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 2661;
RX MEDLINE=96337999; PubMed=8688087;
RA Suttton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
  Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
  Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
  RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
  Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
  RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
  RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
  RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
  jannaschii.";
  RL Science 273:1058-1073(1996).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
DR EMBL; U67602; AAB99649.1; -.
DR TIGR; MJ1626; -.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 7 27 POTENTIAL.
FT TRANSMEM 51 71 POTENTIAL.
SQ SEQUENCE 765 AA; 89606 MW; 056EEAA4FEF9B098 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 765;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTEEOKLI 39
  |||||
Db 750 TTEEOKLI 757

RESULT 22
Q9K2M5
ID Q9K2M5 PRELIMINARY; PRT; 59 AA.
AC Q9K2M5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE REPA PROTEIN (FRAGMENT).
GN REPA.
OS Pseudomonas syringae.
OG Plasmid p5D425A, Plasmid pBBS325A, and Plasmid pB8617A.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
  Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5D425, BBS32-5, AND B86-17;
RA Sesma A., Sundin G.W., Murillo J.;
  RT "Phylogeny of the replication regions of pPT23A-like plasmids from
  Pseudomonas syringae suggests they have a limited horizontal
  mobility.";
  RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5D425, BBS32-5, AND B86-17;
RX MEDLINE=99173737; PubMed=10075415;
RA Gibbon M.J., Sesma A., Canal A., Wood J.R., Hidalgo E., Brown J.,
  RA Vivian A., Murillo J.;
  RT "Replication regions from plant-pathogenic Pseudomonas syringae

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RT plasmids are similar to Cole2-replicon.;

RL Microbiology 145:325-334(1999).

DR EMBL; AJ277001; CAB83236.1; -.

DR EMBL; AJ276999; CAB83234.1; -.

DR EMBL; AJ277000; CAB83235.1; -.

KW Plasmid.

FT NON_TER 59

SQ SEQUENCE 59 AA; 6349 MW; D32EA71AE0899432 CRC64;

Query Match 5.1%; Score 7; DB 2; Length 59;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LATSPTA 26

Db 11 LATSPTA 17

RESULT 23

Q9XJP0

ID Q9XJP0 PRELIMINARY; PRT; 132 AA.

AC Q9XJP0;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DE P12 (FRAGMENT).

OS bacteriophage phi-7.

OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.

OX NCBI_TaxID=90888;

RN [1]

RP SEQUENCE FROM N.A.

RA Mindich L., Qiao X., Qiao J., Romantschuk M., Hoogstraten D.;

RT "Isolation of additional bacteriophages with genomes of segmented

RT double-stranded RNA.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF125682; AAD22566.1; -.

FT NON_TER 132

SQ SEQUENCE 132 AA; 13255 MW; F23726E1DCD60FC0 CRC64;

Query Match 5.1%; Score 7; DB 9; Length 132;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVAVVLG 19

Db 44 AVAVVLG 50

RESULT 24

Q9HL70

ID Q9HL70 PRELIMINARY; PRT; 152 AA.

AC Q9HL70;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE PROBABLE 50S RIBOSOMAL PROTEIN L11.

GN TA0361.

OS Thermoplasma acidophilum.

OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;

OC Thermoplasma.

OX NCBI_TaxID=2303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DSM 1728;

RX MEDLINE=20479972; PubMed=11029001;

RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,

RA Meves H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;

RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma

RT acidophilum.";

RL Nature 407:508-513(2000).

DR EMBL; AL445064; CAC11505.1; -.

DR InterPro: IPR000911; -.

DR Pfam; PF00298; Ribosomal_L11; 1.

DR ProDom; PD001367; -; 1.

KW Ribosomal protein.

SQ SEQUENCE 152 AA; 15966 MW; 45A3779B11D7DB21 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 152;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 EGGKATT 33

Db 6 EGGKATT 12

RESULT 25

Q9HPS5

ID Q9HPS5 PRELIMINARY; PRT; 189 AA.

AC Q9HPS5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE VNG1492C.

GN VNG1492C.

OS Halobacterium sp. (strain NRC-1).

OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;

OC Halobacterium.

OX NCBI_TaxID=64091;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20504483; PubMed=11016950;

RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Ledthauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

RT "Genome sequence of Halobacterium species NRC-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

DR EMBL; AE005064; AAG19792.1; -.

SQ SEQUENCE 189 AA; 20104 MW; 9CDD64D566A50484 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 189;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 RAAMATT 53

Db 82 RAAMATT 88

RESULT 26

Q9XE16

ID Q9XE16 PRELIMINARY; PRT; 203 AA.

AC Q9XE16;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DE HYPOTHETICAL 22.7 KDA PROTEIN.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;

OC Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa Nipponbare(GA3) genomic DNA, chromosome 2, PAC

RT clone:p0437H03 (contig b).";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP000367; BAA82385.1; -;
 SQ Hypothetical protein.
 KW SEQUENCE 203 AA; 22666 MW; E05D4A74A162DA9F CRC64;

Query Match 5.1%; Score 7; DB 10; Length 203;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 48 AMATTA 54
 Db 3 AMATTA 9
 |||||

RESULT 27
 P93029 PRELIMINARY; PRT; 209 AA.
 AC P93029;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PUTATIVE CYS3HIS ZINC FINGER PROTEIN ATCTH.
 GN CTH.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Fett-Neto A.G., McClung C.R.;
 RL Plant Physiol. 0:0-0(0).
 DR EMBL; U81238; AB68046.1; -;
 DR Mendel; 7157; Arath;I540;7157.
 DR InterPro; IPR000571; -;
 DR SMART; SM00356; ZnF_C3H1; 1.
 SQ SEQUENCE 209 AA; 23478 MW; F59DDF8A0408B6A5 CRC64;

Query Match 5.1%; Score 7; DB 10; Length 209;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 GLATSPT 25
 Db 101 GLATSPT 107
 |||||

RESULT 28
 Q53627 PRELIMINARY; PRT; 233 AA.
 ID Q53627;
 AC Q53627;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1997 (TREMBLrel. 03, Last annotation update)
 DE MEMBRANE PROTEIN INVOLVED IN MITHRAMYCIN RESISTANCE.
 GN MTRB.
 OS Streptomyces argillaceus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=41951;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12956;
 RX MEDLINE=96335144; PubMed=8757400;
 RA Fernandez E., Lombe F., Mendez C., Salas J.A.;
 RT "An ABC transporter is essential for resistance to the antitumor agent
 mithramycin in the producer Streptomyces argillaceus.";
 RL Mol. Gen. Genet. 251:692-698(1996).
 DR EMBL; U43537; AAC44358.1; -;

SQ SEQUENCE 233 AA; 25138 MW; 3BC885B35809A215 CRC64;

Query Match 5.1%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 14 VAVVLGL 20
 Db 210 VAVVLGL 216
 |||||

RESULT 29
 Q9UD91 PRELIMINARY; PRT; 297 AA.
 ID Q9UD91;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CALDESMON (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94043679; PubMed=8227296;
 RA Huber P.A., Redwood C.S., Avent N.D., Tanner M.J., Marston S.B.;
 RT "Identification of functioning regulatory sites and a new myosin
 binding site in the C-terminal 288 amino acids of caldesmon expressed
 from a human clone.";
 RL J. Muscle Res. Cell. Motil. 14:385-391(1993).
 DR InterPro; IPR000075; -;
 DR PRINTS; PR01076; CALDESMON.
 DR PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
 SQ SEQUENCE 297 AA; 33675 MW; E292C364E00E5D66 CRC64;

Query Match 5.1%; Score 7; DB 4; Length 297;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 71 VSKRNL 77
 Db 276 VSKRNL 282
 |||||

RESULT 30
 Q9XF24 PRELIMINARY; PRT; 301 AA.
 ID Q9XF24;
 AC Q9XF24;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE POLLEN ALLERGEN LOL P VA PRECURSOR.
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Lolium.
 OX NCBI_TaxID=4522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94085783; PubMed=8262382;
 RA Ong E.K., Griffith I.J., Knox R.B., Singh M.B.;
 RT "Cloning of a cDNA encoding a group-V (group-IX) allergen isoform from
 rye-grass pollen that demonstrates specific antigenic
 immunoreactivity.";
 RL Gene 134:235-240(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ong K.O., Griffith I.J., Knox R.B., Singh M.B.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF128442; RAD20386.1; -;

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DR InterPro; IPR000104; -
DR InterPro; IPR001778; -
DR InterPro; IPR002914; -
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00308; ANTIFREEZEI.
DR PRINTS; PR00833; POAALLERGEN.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 301 POLLEN ALLERGEN LOL P VA.
SQ SEQUENCE 301 AA; 29767 MW; 0EADA8CD711D7DA7 CRC64;

Query Match      5.1%; Score 7; DB 10; Length 301;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 EVHAVKP 136
Db 151 EVHAVKP 157

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Search completed: November 19, 2001, 13:12:30
Job time: 180 sec